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Sequence

Sequence 1, Appl Sequence 2128, Ap

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TITIGAAAGGATATTTTTCGCTCCTATTCAAATACTGTATTTTTACCAAAAAACTGTAT 180 TITTGAAAGGATATTTTTCGCTCCTATTCAAATACTGTATTTTTACCAAAAAAACTGTAT 180 TITTGCTAACTCTCAACTTTTTTTTTTTTTTTTTTTTTTT	1021 TAATTATTTTACTCTTTATTTTCTCTCTATCCTCTTTTTCTCTTATTTCCATATTT 1080 1081 ACACTCCAAAATTGGGGCATGCCTTTATCACTACTCTCTCT


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; PRIOR FILING DATE: 2003-
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: Patentin versi;
; SEQ ID NO 3
; LENGTH: 2012
; TYPE: DNA
; ORGANISM: Glycine max
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SOFTWARE: PatentIn version 3.3
SEQ ID NO 95
LENGTH: 12456
TYPE: DNA
ORGANISM: Artificial Sequence
                                  FEATURE:
OTHER INFORMATION: plasmid
FEATURE:
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LOCATION: (1201)..(1201);
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    -AAAAAAAAAAAAAAAAAGATCATTTTGAAAGGATATTTTTCGCTCCTATTCAAATAC

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                                           Length 12456;
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                                        Score 1961.4; DB 22; Lengt
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                                        Query Match
Best Local Similarity 99.8
Matches 1974; Conservative
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US-10-985-254-95/c
is Sequence 95, Application US/10985254
is Publication No. US20050132442A1
is GENERAL INFORMATION:
is APPLICANT: E1. dubont de Nemours and Co., Inc.
is APPLICANT: Vadav, Narendra
is APPLICANT: Damude, Howard
is TITLE OF INVENTION: DELTA 15 DESATURASES SUITABLE FOR ALTERING LEVELS OF
it TITLE OF INVENTION: POLYUNSATURATED FATTY ACIDS IN OLEAGINOUS YEAST
if TITLE OF INVENTION: US/10/985, 254
is CURRENT FILING DATE: 2004-11-10
is PRIOR FILING DATE: 2003-11-12
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Oy 1956 AAATGAATTCACATAGCTGAGAGAAAAGGAAAGGTTAACTAAGAAGCAATACTTCA 2012 	RESULT 7 US-10-776-889-13 Sequence 13, Application US/10776889 Publication No. US20040158052A1 GENERAL INFORMATION: APPLICANT: Liu, Zhan-Bin APPLICANT: Kinney, Anthony	; FILE OF INVENTION: Seed Specific Promoters ; FILE PEPERBOCE: BB1531 US NA ; CURRENT APPLICATION NUMBER: US/10/776,889 ; CURRENT FILING DATE: 2004-02-11	; NUMBER OF SEQ 1D NOS: 22 ; SOFTWARE: Microsoft Office 97 ; SEQ 1D NO 13 ; LENGTH 1883		Query Match 93.6%; Score 1883; DB 19; Length 1883; Best Local Similarity 100.0%; Pred. No. 2.6e-226; Matches 1883; Conservative 0; Mismatches 0; Indels 0; Gaps		190 ACTCTCAAGCTTTGTTTTTCGCTTCGACTCTCATATTCCTTCATATGCCAATCACTCT				Oy 430 TGACTATITIGGCTTTGACTCCAACACTGGCCCGTACATCCGTCCTCATTACATGAAA 489 101	490 AGAATATTGTTTATATTGTTAATTAAAAATATTGTCCCTTCTAAATTTTCATATGTTA 	Oy 550 ATTATTATATTACTTTTTCCCATTCCATTACTTTCAAATTATT	OY 610 TATGTAAAGTACATTATATTTTTGCTATATACTTTAAATATTGTAAATTATTAAAAAAG 669 	Qy 670 ACTGATATGAAAATTTATTCTTTTAAAGCTATATCATTTTATATATA	Oy 730 CTITICATITICIATICAATITAABAAGAAAAAATITIGTAAATITITATATIC 789	790 AATTTATAAAAATATTTTACTTTATATGTTTTTTCACATTTTTGTTAAACAAATCATATC
876 CAGTGAGTAATAAGTGATGAGAAAAAATGTGTTATTTCCTAAAAAAAA	936 AIGTATCTACTCTATTTCATCTATCTCATTTCTCTTTATCTCTTTTTT	1056 CCCTCTCTTATTTCCACTCATATACACTCCAAAATTGGGGCATGCCTTTATCACTACT 1115 	1116 CTATCTCCACTAAATCATTTAAATGAAACTGAAAAGCATTGGCAAGTCTCCTCCCCT 1175 	1176 CCTCAAGTGATTTCCAACTCAGCATTGGCATTGATTCAGTATATCTATTGCATGT 1235	1236 GTAAAAGTCTTTCCACAATACATAACTATTAATTAATCTTAAATAAATAAAGGATAAAAT 1295 	1296 ATTITITITCTICATAAATTAAATAIGITATTITITITITIGITAGAIGIATATTCGAATA 1355 	1356 AATCTAAATATGATAATGATTTTTATATTGATTAAACATATAATCAATATTAATTT 1415 	1416 GATATTTTTTATATAGGTTGTACACATAATTTTATAAGGATAAAAAATATGATAAAAAT 1475 	1476 aaattttaaatattttatatttacgagaaaaaaatatttagccataaataa	1536 CAGCATATTTTACAACCTTAGTAATTCATAAATTCCTATATGTATATTTGAAATTAAAAA 1595 	CAGATAATCGTTAAGGGAAGGAATCCTACGTCATCTTTGCCATTGTTTTTCATGCCAAA	CAGAAAGGGACGAAAACCTCCTCACCATGAATCACTCTTCACACCATTTTTACTAGCAA 	1716 ACAAGTCTCAACACTGAAGCCAGCTCTCTTTCGTTTTTTACAACACTTTCTTT	AATAGTAGTATTTTTTTTCACATGATTTATTAACGTGCCAAAACATGCTTATTGAATAG 	AGIGCACATTIGIAAIGIACIACTAATTAGAACAIGAAAAAGCAITGITCIAACACGATA 1895 [HIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	ATCCTGTGAAGGCGTTAACTCCAAAGATCCCATTTCACTATAAATTGTGACGAAGCA 1955	10571 AFCCFGFGAAGGCGFFAACFCCAAFFFCAAFFFCACFAFAFAAAFFGFGACGAAAGCA 10512

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Qy 1974 GAGAGAAAGGAAAGGTTAACTAAGAAGCAATACTTCA 2012	RESULT 9 US-10-776-889-15 ; Sequence 15, Application US/10776889 ; Publication No. US20040158052A1 ; GENERAL INFORMATION: ; APPLICANT: Liu, Zhan-Bin ; APPLICANT: Anthony, Anthony, Anthony, Anthony, Anthony, Anthony, Anthony	TILE OF LIVERILOR: SEED SPECIFIC FIGHERER FILE REFERENCE: BEISJI US NA CURRENT APPLICATION NUMBER: US/10/776,889 CURRENT FILING DATE: 2004-02-11 NUMBER OF SEO ID NOS: 22	; SOFTWARE: Microsoft Office 97 ; SEQ ID NO 15 ; LENGTH: 1553 ; TYPE: DNA ; ORGANISM: Glycine max	US-10-776-889-15	Qy 460 CCCGGTACATCGTCCTATACATGAAAAGAAATATTGTTTATATTAAAAA 519	TATTGTCCCTTCTAAATTTTCATATGTTAATTATTATATTACTTTTTTTCTCTATTCTAT 57 	580 TAGTICTATTITGAAATTATTATTATTATGCATATGGTAAAGTACATTATATTTTTGCTATATT 	640 ACTIVARIATICIAAATIATIAAAAAAGACIGAIATGAAAATITATICITITITAAGA 69 181 ACTIVAAATATICIAAATATIATIAAAAAAGACIGATATGAAAATITATITITIAAGA 24	700 CTATATCATTTATATACTTTTCCTTTCCTTTCCTTTTCCTATTCATTTAATA 75 [1]	760 AGAARTAATTITGRAATTITIATITATGAATTIRIAAAAATATITTAGTITTARGIT 81 	820 TTTTCACATTTTGCTAAACAAATCATATCATTATGATTGAAAGAGGGAAATTGACAGT 87 	Qy 880 GAGTAATAAGTGATGAGAAAAAATGTGTTATTTCCTAAAAAAACCTAAACAACATGT 939	Qy 940 ATCTACTCTATTTCATCTATCTCTCTATTTTCTCTTTATCTCTTTATTT 999	Oy 1000 TTTATCATATCACATTAATTATTTTACTCTCTTTATTTTTCTCTCTATCCCT 1059	OY 1060 CTCTTATTCCACTCATATACACTCCAAAATTGGGGCATGCCTTTATCACTACTTAT 1119
894 GAGAAAAAATGTGTTATTTCCTAAAAAACCTAAACAAACA	954 TCATCTATCTCTCATTTCTTTTTCTCTTTATCTTTTTTTT	1074 CATATATACACTCCAAAATTGGGGCATGCCTTTATCACTACTCTATCTCCTCCACTAAAT 1133 	1134 CATTTAAATGAAAAGCATTGGCAAGTCTCCTCCCCCCAAGTGATTTCCAAC 1193		AATTAAAATATGTTATTTTTTTTTTTAGATGAATAAATGTAAAAATGTAAAAA 137 AATTAAAATATGTTATTTTTTTTTTTGTTAGATGAATAAATGTAAA 108 AATTAAAATATGTTATTTTTTTTTTTTTTTTAAATGAATAAT	TGATTTTTTATATTGATTAAACATATAATCAATATTAAATATGATATTTTTTTATATGG 143 	1434 TTGTACACATAATTTTATAAGGATAAAAATATGATAAAAATAAAT	1494 TATITACGAGAAAAAAAATATITTAGCCATAAATAAATGACCAGCATATITTACAACCT 1553 	1554 TAGTAATTCATAAATTCCTATATGTATATTTGAAATTAAAAACAGATAATCGTTAAGGGA 1613 	aggaatcctacgtcatctcttgccatttgtttttcatgcaacagaaagggacga 	CACCTCACCATGAATCACTCTTCACACCATTTTTACTAGCAAACAAGTCTCAACA 	AGCCAGCTCTCTTTCCGTTTCTTTTACAACACTTTCTTTGAAATAGTAGTATTT 	TCACATGATTTATTAACGTGCCAAAAGATGCTTATTGAATAGAGTGCACATTTGTAATGT 1	ACTACTAATTAGAACATGAAAAGCATTGTTCTAACACGATAATCCTGTGAAGGCGTTAA 1	CTCCAAAGATCCAATTTCACTATAAATTGTGACGAAAGCAAAATGAATTCACATAGCT 197

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                                                         Best Local Similarity 100.
Matches 1367; Conservative
                 TYPE: DNA
ORGANISM: Glycine max
US-10-776-889-16
   SEQ ID NO 16
LENGTH: 1367
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US-10-776-889-16

i Sequence 16, Application US/10776889

i Publication No. US20040158052A1

i GENERAL INFORMATION:

APPLICANT: Liu, Zhan-Bin

TITLE OF INVENTION: Seed Specific Promoters

FILE REFERENCE: BB1531 US NA

CURRENT FILING DATE: 2004-02-11

NUMBER OF SEQ ID NOS: 22

; SOFTWARE: Microsoft Office 97
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                                                            CITCACACCATTITIACTAGCAAACAAGTCICCAACAACTGAAGCCAGCTCTCTTTCCGTT
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Publication No. US20040158052A1
GENERAL INFORMATION:
APPLICANT: Liu, Zhan-Bin
APPLICANT: Liu, Zhan-Bin
TILE OF INVENTION: Seed Specific Promoters
FILE REFERENCE: BB1531 US NA
CURRENT APPLICATION WINGHER: US/10/776,889
CURRENT FILLING DATE: 2004-02-11
NUMBER OF SEQ ID NOS: 22
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Publication No. US20040158052A1
GENERAL INFORMATION:
APPLICANT: Liu, Zhan-Bin
APPLICANT: Kinney, Anthony
ITLE OF INVENTION: Seed Specific Promoters
FILE REFERENCE: BB1531 US NA
CURRENT FILING DATE: 2004-02-11
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Microsoft Office 97
SEQ ID NO 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Glycine max
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US-10-776-889-17
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US-10-776-889-17
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                                                                                                                                                                         Sequence 19, Application US/10776889; Sequence 19, Application US/10776889; Publication No. US20040158052A1; GENERAL INFORMATION:
APPLICANT: Liu, Zhan-Bin
APPLICANT: Kinney, Anthony; TITLE OF INVENTION: Seed Specific Promoters; FILE REFERENCE: BB1531 US NA; CURRENT APPLICATION NUMBER: US/10/776,889; CURRENT FILING DATE: 2004-02-11; NUMBER OF SEQ ID NOS: 22; SOCTWARRE: Microsoft Office 97; SEQ ID NO 19
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; ORGANISM: Glycine max
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                                                                                                                                                 Length 967;
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                                                                                                                                             Query Match 48.1%; Score 967; DB 19; L
Best Local Similarity 100.0%; Pred. No. 6.8e-112;
Matches 967; Conservative 0; Mismatches 0;
SOFTWARE: Microsoft Office
SEQ ID NO 18
LENGTH: 967
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                                                           ; TYPE: DNA
; ORGANISM: Glycine
US-10-776-889-18
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100.0%; Pred. No. 4.5e-64;
tive 0; Mismatches 0;
                                                                                                                                           Sequence 20, Application US/10776889
Publication No. US20040158052A1
GENERAL INFORMATION:
APPLICANT: Liu, Zhan-Bin
APPLICANT: Kinney, Anthony
TITLE OF INVENTION: Seed Specific Promoters
FILE REFERENCE BB1531 US NA
CURRENT APPLICATION NUMBER: US/10/776,889
CURRENT FILING DATE: 2004-02-11
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Microsoft Office 97
SEQ ID NO 20
LENGTH: 584
                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 100.
Matches 584; Conservative
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CORGANISM: Glycine max
US-10-776-889-20
                                                                                                                       RESULT 14
US-10-776-889-20
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100.0%; Pred. No. 3.1e-44;
iive 0; Mismatches 0;
RESULT 15
US-10-776-889-21
Sequence 21, Application US/10776889
Publication No. US20040158052A1
GENERAL INFORMATION:
APPLICANT: Liu, Zhan-Bin
TITLE OF INVENTION: Seed Specific Promoters
FILE REFERENCE: BB1531 US NA
CURRENT APPLICATION NUMBER: US/10/776,889
CURRENT PILING DATE: 2004-02-11
NUMBER OF SEQ ID NOS: 22
SEQ ID NO 21
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Best Local Similarity 100.0°
Matches 425; Conservative
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TYPE: DNA
CRGANISM: Glycine max
US-10-776-889-21
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GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.	
OM nucleic - nucleic search, using sw model	
Run on: September 1, 2005, 22:19:32 ; Search time 6107.49 Seconds (without alignments) 15962.684 Million cell updates/sec	onds tes/sec
Title: US-10-776-889-1 Perfect score: 2012 Sequence: 1 atcttaggcccttgattataaactaagaagcaatacttca 2012	012
Scoring table: IDENTITY NUC Gapext 1.0	
Searched: 4708233 segs, 24227607955 residues	
Total number of hits satisfying chosen parameters: 9416466	
Minimum DB seq length: 0 Maximum DB seq length: 200000000	
Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	
Database : GenEmbl:* 1: 9b ba:* 2: 9b htg:* 3: 9b in:* 4: 9b om:* 5: 9b ow:* 6: 9b pat:* 7: 9b ph:* 8: 9b ph:* 10: 9b r:* 11: 9b sts:* 11: 9b sts:* 13: 9b on:* 14: 9b vi:*	

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	ដូ	Homo sapi	Sequence	Human DNA	Danio rer	Plasmodiu	Plasmodiu	Plasmodiu	Gorilla g	Plasmodiu	Danio rer	Danio rer	Ното варі	Homo sapi	Danio rer	Homo sapi	Rattus no	Homo. sapi	Homo sapi	Human DNA
	Description	AC069435	AX344555	AL592166	CR626936	AE001398	AC005504	AC004157	AC149549	AE014849	CR626872	CR392006	AL132672	AC091214	CR759967	AC084128	AC125567	AC098822	AC137629	AL627107
	ID	AC069435	AX344555	ALS92166	CR626936	AE001398	AC005504	AC004157	AC149549	AE014849	CR626872	CR392006	HSJ282H10	AC091214	CR759967	AC084128	AC125567	AC098822	AC137629	AL627107
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de	Query Match	8.5	8.4	8.4	8.1	8.0	8.0	8.0	8.0	8.0	7.9	7.9	7.9	7.9	7.9	7.9	7.8	7.8	7.8	7.8
	Score	170.2	170	168.2	162	161.2	160.4	160.4	160.4	160.4	159.8	159.6	158.6	158.4	158.4	158	157.8	157.8	157.6	156.8
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	Result No.	υ		υ	υ	υ	υ	υ	υ		υ	υ			υ			U	U	U

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	21	156	7.8	15548	ø	AX347057	AX347057 Sequence	ence
U	22	155.2	•	148937	~	CR361568	CR361568 Danio re	o rer
	23	155.2	7.7	348174	٣	CR382399	CR382399 Plas	Plasmodiu
υ	24	154.6	•	172777	~	CR847809	6	Danio rer
	25	154.6	7.7	176704	~	CR628364	CR628364 Danio	o rer
U	56	154.4	•	170143	~	AC048384	AC048384 Homo	sapi
	27	154.2	•	171537	~	CR762390	0	o rer
υ	28	154.2	7.7	174198	~	CR762438	CR762438 Danio	o rer
	53	154	7.7	169800	~	CR847821	_	o rer
	30	154		254050	٣	PFA929358		Plasmodiu
υ	31	154	7.7	313050	٣	PFA929352	AL929352 Plas	Plasmodiu
	32	153.6		186165	σ	AC112187	AC112187 Homo	sapi
	33	153.4		159618	σ	AC096750	AC096750 Homo	
	34	153.2		157467	~	CR792423	CR792423 Danio	o rer
	35	153	7.6	9	~	CR376750	CR376750 Danio	o rer
υ	36	152.8		154044	~	CR786570	CR786570 Danio	o rer
	37	152.8		214709	~	CR749183	CR749183 Danio	o rer
υ	38	152.8		228431	~	CR788237		o rer
	39	152.6		210218	~	CRS55304	4	o rer
υ	40	152.6		210871	~	CR759970	CR759970 Danio	o rer
	41	152.4		148075	σ	AC110014	AC110014 Homo	sapi
υ	42	152.4		155106	σ	AC104069		
	43	151.8		251237	~	CR812792	2 Dani	n
	44	151.6	7.5	178785	σ	AC068139	AC068139 Homo	sapi
υ	45	151.6		227073	~	CR846086	CR846086 Danic	

ALIGNMEN

RESULT 1
AC069415
AC069415
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BOD ospiens 3 BAC RP11-38411 (Roswell Park Cancer Institute Human BAC Library) complete sequence.
ACC65310 AC069415
ACC65310 GI:20340410
ACC65415
A

(bases 1 to 111861)

Jnpublished lorley, K.C.

JOURNAL

TITLE

Direct Submission

AUTHORS TITLE JOURNAL

Direct Submission

Worley, K.C.

REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS TITLE

JOURNAL

COMMENT

Wu, Y.F., Zhou, J., Gibbs, R. Direct Submission

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: .2005
note="overlaps bases 165307. .167311 of clone AC073895"
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9667. 9968
/rpt_femily="AluSx"
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/rpt_family="MIR" 15626)
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                                                                                                                                                                                                                                                                                     /rpt_family="LTR33"
882. 2011
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complement(11197 .1
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13104. .13257
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /rpt_family="MER92C"
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3934. .9209
                                                                                                               /chromosome="3
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1444<u>6</u>.
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Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L.L., Quilles, M., Ren, Y., Rives, M., Srojas, A., Rojubokan, I., Rolfe, M., Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I., Sodergren, E., Sonake, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, F., Tang, H., Tansey, J., Taylor, C., Taylor, F., Telfrod, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wang, G., Wang, S., Ward-Moore, S., Walliamson, A., Maeczyk, R., Wooden, S., Williamson, A., Maeczyk, R., Wooden, S., Worley, K., Wu, C., Wu, Y., R., Zhou, J., Zorrilla, S., Naylor, S.L., Weinstock, G. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.
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Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:338-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice aites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Worley, K.C.
Submission
Submissio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (30-MAY-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases 1 to 111861)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (30-APR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
4 (bases 1 to 111861)
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ANNOTATION OF FEATURES:

QUALSTAT-REPORT source FEATURES

Location/Qualifiers 1. .111861

01-FEB-2002

PAT

549

Gaps

4.

Indels

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/note="chemically treated genomic DNA (Homo appiens) -Original length of seq 1: 3.673778 <223>-split as splits as follows.-seq 01 0.000.001 TO 0.349.980-seq 02 0.300.001 649.980-seq 02 0.300.001 1.249.980-seq 03 600.001 1.949.980-seq 06 1.500.001 1.249.980-seq 07 1.800.001 1.549.980-seq 06 1.500.001 1.499.980-seq 07 1.800.001 2.149.980-seq 08 2.100.001 2.449.980-seq 09 2.400.001 2.149.980-seq 10 2.700.001 3.049.980-seq 11 3.000.001 3.349.980-seq 12 3.300.001 3.649.980-seq 13 3.000.001 3.649.980-seq 12 3.300.001 3.649.980-seq 14 1.200.001 2.149.980-seq 19 1.500.001 1.849.980-seq 18 1.200.001 1.549.980-seq 19 1.500.001 1.849.980-seq 22 2.400.001 2.149.980-seq 22 2.400.001 2.149.980-seq 22 2.700.001 2.749.980-seq 23 2.700.001 3.049.980-seq 24 3.000.001 3.449.980-seq 25 3.300.001 3.649.980-seq 26 3.500.001 3.649.980-seq 26 3.500.001 3.649.980-seq 26 3.500.001
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                                                                                   TATATGATAATGATTTTTTAATTGATTAAACATATAATCAATATTAAATATGATATTTT
                                                                                                           ATTATTATATTACTTTTTTCTCTATTCTATTAGTTCTATTTTCAAATTATTATGCA
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48.8%; Pred. No. 3.6e-11;
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Diagnosis of known genetic parameters within the mhc
Patent: WO 0200933-A 6 03-JAN-2002;
Epigenomics AG (DE)
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
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AX344555
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8.5%; Score 170.2; DB 9; Length
Best Local Similarity 48.6%; Pred. No. 5.1e-11;
Matches 551; Conservative 0; Mismatches 578; Indels
                                                                           /rpt_family="MLTIA1"
complement(21762..22107)
/rpt_family="MLTI1"
22360..22395
                                                                                                                                       /rpt_family="AT_rich"
22559. .22817
/rpt_family="AluSx"
complement(22927. .23015)
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21442. .21725
/rpt_family="GA-rich"
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Libert Submitted (13-MAR-2003) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 18A, UK. E-mail enquiries: hunguery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk on Mar 23, 2003 this sequence version replaced gi:18476714.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Ems. EMBL: Sww.; SWISSPROT; Tr.; TREMBL; Wp.; WORNPEP; Information on the WORNPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        on the WORMPEP database can be found at http://www.anger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at http://www.anger.ac.uk/HGP/Chr1
RP11-269F19 is from the library RPCI-11.1 constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
Human DNA sequence from clone RP11-269F19 on chromosome 1, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone behing a YAC.
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Catarrhini, Hominidae, Homo.
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Pred. No. 9.1e-11;
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Contact: humquery@sanger.ac.uk
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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/clone_lib="RPCI-11.1"
                                                                                                                        Homo sapiens
Bukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
1 (bases 1 to 90550)
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PRI 23-MAR-2003

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90550 bp

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Danio rerio clone DKEY-107122, WORKING DRAFT SEQUENCE, 5 unordered
pieces:
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                             59412 ATATTCATAATACTTATATTTA-TTTATATTTTATATTTTATATATTTTATATTT
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ACCESSION

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Submitted (08-AUG-2004) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Aug 9, 2004 this sequence version replaced gi:50896321.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Statinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 17968)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Assembly program: XGAP4, version 4.5
Chemistry: Dye-terminator; 100% of reads
Consensus quality: 177410 bases at least Q40
Consensus quality: 177759 bases at least Q30
Consensus quality: 178052 bases at least Q30
Insert size: 179268; sum-of-contigs
Insert size: 1793635; 3.1% error; agarose-fp
Quality coverage: 9.22x in Q20 bases; sum-of-contigs Quality
coverage: 9.90x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            * NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as as soon as it is available and the accession number will be preserved.
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179668: contig of 49474 bp in length
Location/Qualifiers
1. 179668
/organism="Danio rerio"
/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="DKEY-107122"
/clone="DKEY-107122"
/location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5950: contig of 5950 bp in length
6050: gap of 100 bp
72517: contig of 66467 bp in length
72617: gap of 100 bp
87634: contig of 15017 bp in length
87734: gap of 100 bp
130094: contig of 42360 bp in length
130194: gap of 100 bp
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87735. 130094
/note=assembly_fragment:00264"
130195. 179668
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1. .5950
/note="assembly_fragment:00021
fragment_chain:1"
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/note="assembly fragment:01524
[fragment_chain:<u>1</u>"
72618. .87634
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ragment_chain:1"
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Place of the point of the point of the point of the point of the complete sequence.
AE001398 AE001362
AE001398.1 GI:3845197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genome sequence of the human malaria parasite Plasmodium falciparum
Nature 419, 498-511 (2002)
3 (bases 1 to 14867)
                                                                                                                                                                                                                                             Plasmodium falciparum 3D7

Bukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

Bukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

Bukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

Gardner, M.J., Tettelin, H., Carucci, D.J., Cummings, L.M., Aravind, L.,

Koonin, E.V., Shallom, S., Mason, T., Yu, K., Fujii, C., Pederson, J.,

Shen, K., Jing, J., Aston, C., Lai, Z., Schwartz, D.C., Pertea, M.,

Salzberg, S., Zhou, L., Sutton, G.G., Clayton, R., White, O.,

Smith, H.O., Franer, C.M., Adams, M.D., Venter, J.C. and Hoffman, S.L.

Chromosome 2 sequence of the human malaria parasite Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (02-OCT-2002) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA Location/Qualifiers
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                                               72147 TATATATATATATATATATATATA 72122
                  1576 TGTATATTTGAAATTAAAACAGATA 1601
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/isolate="3D7"
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complement(378. .423)
/note="AT_rich"
/rpt_type=tandem
complement(479. .503)
/note="AT_rich"
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/rpt type=tandem
complement (65. .137)
/note="AT_rich"
/rpt type=tandem
complement (178. .211)
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                                  498 IGTTTATATTCTTAATTAAAATATTGTCCCTTCTAAATTTTTCATATAGTTAATTATTAT
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                                                                                                 558 ATTACTTTTTCTCTATTCTATTAGTTCTATTTTCAAATTATTATTATGCATATGTAAA
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                                                                                                                                                                                                                                                                                                738 TCATTITCTATICAATTIAAIAAGAAAIAAAT-ITTGIAAATTITITATTATCAAITTAT
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   Gaps
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Matches 498;
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; *** SEQUENCING IN PROGRESS
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Submitted (21-AUG-1998) Stanford DNA Sequencing and Technology
Center. Stanford University, 855 California Avenue, Palo Alto, 94304, USA
On Apr 2, 1999 this sequence version replaced gi:4337172.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 73851 CATTİTAAİTAAAATAACCATTİATTAAİTAACTİAATTAAİATAATAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      389 TGAATTTTTTCGAATAGTCATGCAGTGCATTAATTTCCCCGTGACTATTTTGGCTTTGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          155 CTGTATTTTTACCAAAAACTGTATTTTTCCTACACTCTCAAGCTTTGTTTTTCGCTTC
                                                                                                                Eukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium.
1 (bases 1 to 104992)
                                                                                                                                                                                                                                                                               On Apr 2, 1999 this sequence version replaced gi:4337172.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 3 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 104992;
                                                         AC005504.3 GI:4558584
HTG: HTGS PHASEL.
Plasmodium falciparum (malaria parasite P. falciparum)
Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                    S8642: contig of S8642 bp in length
58842: gap of unknown length
91011: contig of 32169 bp in length
91211: gap of unknown length
104992: contig of 13781 bp in length.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Plasmodium falciparum"
/mol_type="genomic DNA"
/db_xref="taxon:5833"
/chromosome="12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches 816;
                                                                                                                                                                              Plasmodium falciparum 3D7 chromosome 12
               Plasmodium falciparum chromosome 12,
 104992 bp
                                                                                                                                                 Hyman, R.W., Fung, B.L., Qin, F., and Davis, R.W.
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                               unordered pieces.
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Query Match
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72606 TATATATTTAATTTTAATATTTTTAAATTAATTATAATGATTTAATTTAATTTAATTTA
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2 (bases 1 to 169546)
Hyman.R.W., Qin,F., Fung,E.L., Conway,A.B. and Davis,R.W.
Direct Submission
Submitted (19-FBB-1998) Stanford DNA Sequencing and Technology
Center, Stanford University, 855 California Avenue, Palo Alto, 94304, USA
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HTG; HTGS_PHASE1.
Plasmodium falciparum (malaria parasite P. falciparum)
Plasmodium falciparum
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 169546)
Hyman, R.W., Pung, E.L., Qin, F., Rowley, D., Mao, J., Tamaki, T., Rurdi, O.B., Conway, A.B. and Davis, R.W.
Plasmodium falciparum 3D7 chromosome 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             on Aug 12, 2000 this sequence version replaced gi:8810447.

* NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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23467 23666: gap of unknown length
23667 169546: contig of 145880 bp in length.
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ilarity 46.6%; Pred. No. 5.5e-10;
Conservative 0; Mismatches 816;
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/clone="3D7"
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	AC149549 M Gorilla gorilla gorilla clone CH255-73 ordered pieces. AC149549 AC149549. AC149549. AC149549. AC149549. AC149549. GORILLA GORILLA GORILLA GORILLA GORILLA GORILLA GORILLA GORILLA GORILLA GORILLA MANAMALIA: MALREN, DENALA MALREN, D.L., OSOEGWAW, K., Friedman, C., MALONELIA, A., APALE, K., BOUFFARG, G.G., Brinkley, C., Brooks, S., COLEMAN, H., DAKI, N., HO, SL., HI, P., HI KATLINS, E., KİM, H., KWONG, P., LATIC, P.	legaspi,R., Madden,M., Maduro,Q.L., Masseri,B., Medowell,J., Park,M., Portnoy,M.E., Prasad,A., Purings,M.E., Prasad,A., Purings,M.E., Prasad,A., Purings,B., McDowell,J., Park,M., Portnoy,M.E., Prasad,A., Purings,J.W., Thomas,D.W., Tsipouri,V., Tomas,J.W., Thomas,D.W., Tsipouri,V., Young,A. and Green,E.D. NISC Comparative Sequencing Initiative Unpublished 2 (bases 1 to 202169) 3 (bases 1 to 202169) 6 Green,E.D. 6 Growemont Circle, Gaithersburg, MD 206 6 Growemont Circle, Gaithersburg, MD 206 7 Submitted (100-JUN-2004) NIH Intramural Schomitted (30-JUL-2004) NIH Intramural Schomitted (30-JUL-2004) NIH Intramural Schomitted (30-JUL-2004) NIH Intramural Schomitted (30-JUL-2004) NIH Intramural Schomering Conter code: NISC Wabb site: http://www.nisc.nih.gov.conter: NIH Intramural Sequencing Center project name: 073802 The sequence data in this record repreversion of a phase 2 submission. Speciocider and orientation of each sequence established using one or more of the false former individual subclones, overled
8 3 8 3 8 3 8 3 8	RESULT 8 AC149549/C LOCUS DECINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS	TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL COMMENT
331 TGCCTTTCAAAATTATCTGCACCCCCTAGCTATAATCTAACTTAAGTAAG		929 AACAAACATGTATCTACTCTATTTCATCTATTTTTTTTTT
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1,C., de Jong, P.J., Trask, B.J.,
B., Blakesley, R.W.,
B., Chu, G., Coleman, B.,
Hurle, B., Idol, J.R., Jones, C.,
Ic, P., Larson, S., Lee-Lin, S.-Q.,
J., Maduro, V.B., Margulies, E.H.,
J., Maduro, V.B., Margulies, E.H.,
J., Mullikin, J.C., Paguirigan, C.,
Puri, O., Reddix-Dugue, N.,
K., Sison, C., Stantripop, S.,
I.V., Vogt, J.L., Wetherby, K.D., TTATAATGATTTAATTTGATATA 84131 GAGAAAAAAAAT---ATTTTAGCCA 1523 AATTCATAAATTCCTATATGTATT 1583 ATCCTACGTCATCTCTTGCCATTTGT 1643 NNA linear HTG 30-JUL-2004 73E2, WORKING DRAFT SEQUENCE, 6 ita; Vertebrata; Euteleostomi; hini; Hominidae; Gorilla. ral Sequencing Center, 8717 al Sequencing Center, 8717 10877, USA on replaced gi:48427674. epresents an 'enhanced' pecifically, the indicated ence contig has been he following: read-pair erlaps with neighboring eference sequence (e.g., ng Center (111a) 8

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**NOTE: This is a 'working draft' sequence. It currently consists of 6 contigs. Gaps between the contigs are prepresented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

15313 15412: contig of 15312 bp in length 15312: contig of 15312 bp in length 13351 contig of 7282 bp in length 13413 73350: contig of 7282 bp in length 13451 soon of unknown length 13351 contig of 57321 bp in length 13353; contig of 52321 bp in length 13354 13353; gap of unknown length 13354 159871: contig of 2618 bp in length 13354 159871: contig of 2618 bp in length 159972 202169; contig of 42198 bp in length 159972 202169; contig of 42198 bp in length 150016.
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SM Plasmodium falciparum 3D7

Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

E 1 (bases 1 to 250421)

Gardner, M.J., Hall, N., Fung, E., White, O., Berriman, M., Hyman, R.W., Carlton, J.M., Pain, A., Rubherford, K., Salazberg, S.L., Craig, A., James, K., Eisen, J.A., Rutherford, K., Salazberg, S.L., Craig, A., Angiuoli, S., Pertea, M., Allen, J., Selengut, J., Haft, D., Mather, M.W., Vaidya, A.B., Martin, D.M., Fairlamb, A.H., Fraunholz, M.J., Roos, D.S., Ralph, S.A., McFadden, G.I., Cummings, L.M., Subramanian, G.M., Mungall, C., Venter, J.C., Carucci, D.J., Hoffman, S.L., Newbold, C., Davis, R.W., Fraser, C.M. and Barrell, B.
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Nakao, B., Rowley, D., Tamaki, T., Wang, F. and Davis, R.W.
Direct Submission
L Submitted (13-SEP-2002) Stanford Genome Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304, USA
E 3 (bases 1 to 250421)
S Hyman, R.W., Fung, E., Conway, A., Kurdi, O., Mao, J., Miranda, M.,
Nakao, B., Rowley, D., Tamaki, T., Wang, F. and Davis, R.W.
Direct Submission
L Submitted (29-JAN-2003) Stanford Genome Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304, USA
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                                                                                   AE014849 250421 bp DNA linear INV 11-FEB-2003 Plasmodium falciparum 3D7 chromosome 12, section 6 of 9 of the
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Nature 419 (6906), 498-511 (2002)
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25828 ATATTTAATTTTATATATT-----AATTTAATTATATATTTATTTAATTTAATTTAATA 25882
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                                                                   569 CTCTATTCTATTAGTTCTATTTTCAAATTATTATTATGCATATGTAAAGTACATTATAT
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EVEROVPLESSWI PSYLNE I KDI RTI EKDLKLIKKGKS I VNNF I SNONNDHY YONNTKE
EDPKNKKKEONKEONKEOKEI Y NYNSVHI DSHI FY BERNOMDVNK I NDTLHI SN
EHS PERNI KOYDHEY SKETHOEE I I EODKNEENE INSNSNTLLNI I OTNSCDHLSNS
DSDTSNI DDESDSCEONEDEENY SSVHEQEEVKFKGI I PDGI TRKEWCKL VKEONREK
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ICGLRCPYPLULRSNVIWSMIGYIDNACPKMKOLNFDILKWKELYIECICILFRIFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCKLVHADFSEYNLLYFCNHIYIIDVSQSMEHDHPYSLEFLKRDCLNITNFFKKKIGT
IVQQTQPTNLYTQRNEQNVENKTNVDINRVQTNYTNEHVBGYNVEGYNVEGYNVEGYNVEGHN
VEGYNVEGYNVEGHNVEGHNVEGHNVEGYDDTNTIDDKTSHLLPQKDFSKLLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                             locus tag="PFL1490w"
note="HMMPfam hit to PF01163, RIO1/ZK632.3/MJ0444 family,
core 2.2e-55"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VPDAGFYENVEILPLKVLFDFIVSSSLPDDIVYFIENDKKKISLNPYEIIYLQIFGLI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95 AGAAAAAAAAAAAAAGGAAAGGATCATTTTGAAAGGATATTTTCGCTCCTATTCAAATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                product="hypothetical protein"
protein_id="AAN36384.1"
db_xref="G1:23496831"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8.0%; Score 160.4; DB 3
46.6%; Pred. No. 4.8e-10;
                                                                                                                                                                                                                                                                                                                                                                                           locus_tag="PFL1490w"
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738. 7489
7489. 7489
7595. 7643
7595. 7643
7801. 7790=tandem
7801. 7740
7801. 77863
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/rpt_type=tandem
8230. 8255
/rpt_type=tandem
8392. 8485
/rpt_type=tandem
8392. 8639
/rpt_type=tandem
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11322..11373
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9086. .>11884
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Best Local Similarity 46.6
Matches 736; Conservative
repeat_region
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                                                                                                                                              gap of 100 bp
contigo f 1108s bp in length
gap of 100 bp
contig of 6856 bp in length
contig of 9652 bp in length
gap of 100 bp
gap of 100 bp
contig of 3340 bp in length
gap of 100 bp
contig of 4478 bp in length
                                          23452 bp in length 23: contig of 5670 bp in length 33: gap of 100 bp 5: contig of 22632 br
                    100 bp
of 22170 bp in length
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   bp in length
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fragment chain:1"
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/db_xref="taxon:7955"
/clone="DKEY-38L22"
/clone_lib="DanioKey"
   contig
gap of
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175618: 9
180096: 0
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85983:
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                                                  ATTAAATATGATATTTTTTTATATAGGTTGTACACATAATTTTATAAGGATAAAAATAT 1466
                                                                                                               1467 GATAAAAATAAATITITAATTITITATATTTACGAGAAAAAAAAA---ATTTTAGCCA 1523
                                                                                                                                                                                1524 TAAATAAATGACCAGCATATTTTACAACCTTAGTAATTCATAAATTCCTATATGTATAT 1583
                                                                                                                                                                                                                                              1584 TGAAATTAAAAACAGATAATCGTTAAGGGAAGGAATCCTACGTCATCTTGCCATTTGT 1643
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Danio rerio clone DKEY-38L22, *** SEQUENCING IN PROGRESS ***, 12
CR626872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NOTE: This is a 'working draft' sequence. It currently consists of 12 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19704: contig of 19704 bp in length 19804: gap of 100 bp 31589: contig of 11785 bp in length 31689: gap of 100 bp
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HTG; HTGS PHASE1.
Danio rerio (zebrafish)
Danio rerio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
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LOCUS
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KEYWORDS
SOURCE
ORGANISM
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AUTHORS
TITLE
JOURNAL
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HTG 23-AUG-2004

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Submitted (20-AUG-2004) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: 2fish-help@sanger.ac.uk Clone requests: clonerequest@asnger.ac.uk on Aug 23, 2004 this sequence version replaced gi:46879107.
                                                                                                                              Vertebrata; Euteleostomi;
Ostariophysi;
178427 bp DNA linear HTG 23-AUG-20
(P-57F11, *** SEQUENCING IN PROGRESS ***, 9
                                                                                                                                                                                                                                                                                                                                                                                                                   Assembly program: XGAP4; version 4.5
Chemistry: Dye-terminator: 100% of reads
Consensus quality: 173955 bases at least Q40
Consensus quality: 175292 bases at least Q30
Consensus quality: 175292 bases at least Q30
Insert size: 177527; sum-of-contigs
Insert size: 177796; 2.7% error; agarose-fp
Quality coverage: 7.97 x in Q20 bases; sum-of-contigs Quality
coverage: 8.05x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  * NOTE: This is a 'working draft' sequence. It currently consists of 9 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5: contig of 11505 bp in length
1: gap of 100 bp
9: contig of 13326 bp in length
1: gap of 100 bp
9: contig of 6788 bp in length
7: contig of 13349 bp in length
7: gap of 100 bp
7: contig of 33444 bp in length
1: contig of 33444 bp in length
1: gap of 100 bp
9: contig of 33444 bp in length
1: gap of 100 bp
9: contig of 3442 bp in length
2: gap of 100 bp
3: contig of 43724 bp in length
3: gap of 100 bp
3: contig of 43724 bp in length
3: gap of 100 bp
3: contig of 2664 bp in length
3: gap of 100 bp
7: contig of 2664 bp in length
                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata,
Actinopterygii, Neopterygii, Teleostei,
Cyptiniformes, Cyptinidae; Danio.
1 (bases 1 to 176427)
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/note="assembly_fragment:00415
fragment_chain:1"
11406. .24931
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Contact: zfish-help@sanger.ac.uk
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/mol type="genomic DNA"
/db xref="taxon:7955"
/clone="DKEYP-57F11"
              Danio rerio clone DKEYP-57F11, unordered pieces.
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                                                          CR392006.3 GI:51510714
HTG; HTGS PHASE1.
Danio rerio (zebrafish)
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11606. .24931 /note="assembly_fragment:00266

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               fragment chain:1"
31920. 25027
70048
fragment chain:1"
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175764. _178427
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Homo sapiens chromosome 6 clone RP1-282H10 map p22.1-22.3, 5
unordered pieces.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Submitted (09-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 13A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
requests: clonerequest@sanger.ac.uk
On Jun 12, 2001 this sequence version replaced gi:12331282.
                                                                                                                                    1276 AAATAAATAAAGGATAAAATATTTTTTTTTCTTCATAAAATTAAAATATGTTATTTTTG
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                                             TITAGAIGTATATICGAATAAAATCTAAATATATGAT----AATGATITITTATATIGATT
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Web site: http://www.sanger.ac.uk
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HTG; HTGS_PHASE1; HTGS_CANCELLED.
Homo sapiens (human)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

T. (bases I to 143331)

Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C.,
Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Banks, T., Barbaria, J.,
Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Buck, J.,
Burtet, C., Brown, B., Brown, M., Bryant, N.P., Buhay, C.,
Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F.,
Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Cleveland, C.D.,
Cox, C., Chyl, D., Chowdhry, I., Christopoulos, C., Cleveland, C.D.,
Cox, C., Coyle, M.D., Dathorne, S.R., David, M. L., Davis, M. L.,
Dany, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Dersper, H.,
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is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2; Length 120029;
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                                                                                                 23429: contig of 23429 bp in length 23529: gap of 100 bp 63600: contig of 40071 bp in length 63700: gap of 100 bp 100199: contig of 36399 bp in length 100199: gap of 100 bp 10256: contig of 2167 bp in length 102466: gap of 100 bp 102069: contig of 1563 bp in length 102029: contig of 17563 bp in length.
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/note="assembly_fragment:00423

fragment_chain:I"

63701. .100099

/note="assembly_fragment:02685

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100200. ..102366

/note="assembly_fragment:01789"

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/note="assembly_fragment:02341
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.larity 45.6%; Pred. No. 9.8e-10;
Conservative 0; Mismatches 594;

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/note="assembly_fragment:05837
clone_end:SP6

                                                                                                                                                                                                                                                                                                  'organism="Homo sapiens
                                                                                                                                                                                                                                                                                                                  /mol_type="genomic_DN/db_xref="taxon:9606"
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/clone="RP1-282H10"
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Direct Submission
Submitted (04-ARR-2001) Human Genome Sequencing Center, Department
Submitted (04-ARR-2001) Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 143331)
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Submitted (28-JUL-2001) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, IX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (27-JUL-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
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Submitted (12-SEP-2001) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
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Submitted (07-MAR-2002) Human Genome Sequencing Center, Department
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Baylor Plaza, Houston,
4 (bases 1 to 143331)
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Direct Submission
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SEQUENCING READ COVERAGE:Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Incal mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences to the forest and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.
                                                                                                                                                                           CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.
                                                                                                                                                                                                                                                                                                                                                                                 ANNOTATION OF FEATURES:
STSB are identified using ePCR (Genome Res. 7:541-550) searches
of a local database that includes entries from dbSTS, GDB, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QUALITY OF INDIVIDUAL BASES:This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found
of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Jul 17, 2001 this sequence version replaced gi:14578078. INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email gc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.html.
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/note="overlaps bases 1. .2005 of clone AC079409"
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'Tpt_family="LTR16A"

complement (625. 1128)

/rpt_family="Alux"

/rpt_family="LTR107"

/rpt_family="LZ"

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/rpt_family="(TTTTA)n"
7538. .7716
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/standard_name="61535"
12648. .13327
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/db_xref="taxon:9606"
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4457. .5350
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/rpt_family="T-rich"
complement(5374. .60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
1. .143331
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/rpt_family="L1M1"

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17067 ATATATATATATATTTATATATTTTATATATTGATATATATATATATATATTCATATATA 17126
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                    TITCACATTAATTATTTTAACTCTCTTTATTTTTTCTCTCTATCCCTCTCTTATTTCCAC 1072
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Danic rerio clone DKEY-94Pl3, *** SEQUENCING IN PROGRESS ***, 6
unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (10-SEP-2004) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Sep 11, 2004 this sequence version replaced gi:51965792.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cyprinidae; Danio.

1 (Dases 1 to 226108)
Sims,S.
                                                                                                                                                                                                                                                                                                                       1306 CTTCATAAAATTAAAATTATGT-TATTTTTTTTTGTTTAGATGTATATTCGAATAAATTCTAAAT
                                                                                                                                                                                                                       -- TCCAACTCAGCATTGGCATCTGATTGATTCAGTATATCTATTGCATGTGTAAAAGTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Assembly program: XGAP4; version 4.5
Chemistry: Dye-terminator; 100% of reads
Consensus quality: 223262 bases at least Q40
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Web site: http://www.sanger.ac.uk
Contact: zfish.help@aanger.ac.uk
Center project name: zK94P13
Center project name: zK94P13
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HTG; HTGS PHASE1.
Danio rerio (zebrafish)
Danio rerio
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CR759967/c
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DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7.9%; Score 158.4; DB 9; Length 49.8%; Pred. No. 9.8e-10; ive 0; Mismatches 531; Indels
                                                                                                                                                                                                                  function="unresolved tandem repeat"
6264. .16399
                                                                                                                                                                rpt_family="FLAM"
6261. .17570
                                                                                                                                                                                                                                                                                                                                                                                  /rpt_family="(TA)n"
17648...17764
/rpt_family="AluJo/FRAM"
17774...17807
/rpt_family="AT_rich"
17811...18491
/rpt_family="L1"
18494...18612
/rpt_family="L1"
18494...18612
               /rpt_family="AT_rich"
13423. .15610
/rpt_family="LIM1"
15611. .15710
/rpt_family="PLAM_C"
                                                                                                                                                                                                                                                / rpt_family="(TA)n"
16405. 16446
/ rpt_family="AT_rich"
16447. 17315
/ rpt_family="(TA)n"
1736_family="(TA)n"
/ rpt_family="(TA)n"
/ rpt_family="(TA)n"
                                                                                /rpt_family="PLAM_C"
15718. 15889
/rpt_family="(TA)n"
15909. 16212
/rpt_family="(TA)n"
complement (16213, 16
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Best Local Similarity 49.8
Matches 543; Conservative
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Homo sapiens chromosome 8, clone CTD-3118D11, complete sequence.
ACO84128
                                                                                                                                                                                                                                          1036 TCTTTATTTTTTCTCTCTATCCCTCTCTTATTTCCACTCATATATACACTCCAAAATTGG 1095
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Catarrhini; Hominidae; Homo.
                                     AAAAATTTTTACTTTATATGTTTTTTCACATTTTTGTTAAACAAATCATATCATTATGA
                                                                                                      857 TTGAAAGAGGAAATTGACAGTGAGTAATAAGTGATGAGAAAAAAATGTGT-TATTTCC
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Mammalia; Eutheria; Primates; Catarrhini; Hon
1 (Bases I to 129240)
Birren, B., Nucbaum, C. and Lander, E.
Homo sapiens chromosome 9, clone CTD-3118D11
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Consensus quality: 223728 bases at least Q30 Consensus quality: 224330 bases at least Q20 Insert size: 225608; sum-of-contigs Insert size: 219705; 1.4% error; agarose-fp Quality coverage: 11.47x in Q20 bases; sum-of-contigs Quality coverage: 11.63x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                 NOTE: This is a 'working draft' sequence. It currently consists of 6 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2; Length 226108;
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                                                                                                                                                                                                                                                    5476: contig of 5476 bp in length
5576: gap of 100 bp
34821: contig of 29245 bp in length
34921: gap of 100 bp
59976: contig of 24955 bp in length
59976: gap of 100 bp
138475: contig of 78399 bp in length
138475: gap of 100 bp
176166: contig of 37591 bp in length
176166: contig of 37591 bp in length
176166: contig of 49942 bp in length
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Center: Whitehead Institute/ MIT Center for Genome Research
On Jul 30, 2002 this sequence version replaced gi:21306731. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                             Center code: WIBR
Web site. http://www-seq.wi.mit.edu
Conteact: sequence submissions@genome.wi.mit.edu
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69. -855

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Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barran, N., Bastien, V., Bloom, T., Boguslavkiy, L., Burkhgalter, B., Trown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Colling, S., Collymore, A., Cook, A., Cooke, P., Dakrellano, K., Dewar, K., Diaz, J. S., Dodge, S., Faro, S., Ferreira, P., FitzGerald, M., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Mardrim, J., Matchews, C., McCarthy, M., McEwan, P., McKernan, R., Madrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Nell, D., Oliver, J., Peterson, R., Phunkhang, P., Peterre, N., Schauer, S., Schauer, S., Schupback, R., Seaman, S., Severy, P., Spencer, B., Stonger-Thomann, S., Severy, P., Spencer, B., Tradylio, J., Trigilio, J., Vaen, M., Young, C., Washluch, C., Washluch, C., Washluch, C., Washliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Yew, V., Wilson, B., Wu, X., Wyman, D., Yew, M., Salmor, A. and Zody, M. Direct Submission
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Search completed: September 3, 2005, 04:25:16 Job time : 6118.49 secs

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11	425	21.1	425	13	ADR16035	Adri	Adr16035 Soybean a
13	174	8.6	174	13	ADR16036	Adri	6036 Soybean a
13	156	7.8	15548	9	ABL34155	. Abl34	Abl34155 Human imm
14	150.2	7.5	8056	8	ABZ10246	Abz10	Abz10246 Haematopo
12	148.6	7.4	8056	8	AB210246	Abz10246	246 Haematopo
16	147.4	7.3	7597	9	ABL33013	Ab133013	013 Human imm
17	142.2	7.1	8056	æ	AB210100	Abz10	Abz10100 Haematopo
18	136.8	6.8	5286	13	ADS89552	Ads8	Ads89552 Oligonucl
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The present invention describes an oilseed plant (I) that produces mature seeds in which the total seed fatty acid profile comprises at least 1.0%, 5%, 10%, 15%, 10%, 25%, 30%, 25%, 30%, 40%, 60% or more of at least one.

CC 54, 10%, 15%, 20%, 25%, 30%, 40%, 60% or more of at least one polywnsaturated fatty acid having 20 or more carbon atos and 5 or more carbon-carbon double bonds, and ratio of docosahexanoic and confinence acid (IMA.EPA) is 1.100-660:100 or 1:100-110:100, where total seed fatty acid profile further comprises less than 2% arachidonic acid. Also described: (1) seeds (II) obtained from (I); (2) arachidonic acid. Also described: (1) seeds (II) obtained from (I); (2) arachidonic acid. Also described: (1) seeds (II) obtained from (I); (3) arecombinant construct (IV) for alering the total fatty acid profile of mature seeds of an oilseed plant, comprising two or more promoters, where each promoter is operably content of an encellar acid sequence encoding a polypeptide (e.g., delta-4 desaturase, delta-5 desaturase, delta-6 desaturase, delta-6 desaturase, delta-6 desaturase, delta-6 desaturase, delta-6 desaturase, delta-6 desaturase, delta-6 desaturase, delta-6 desaturase, delta-6 desaturase, delta-6 desaturase, delta-6 desaturase, delta-6 desaturase, delta-6 desaturase, delta-6 desaturase, delta-6 desaturase, delta-6 desaturase, delta-6 desaturase, delta-6 desaturase, delta-6 desaturase, delta-6 desaturase, delta-6 desaturase, delta-6 desaturase, delta-6 desaturase, delta-6 desaturase, delta-6 desaturase, delta-6 desaturase, delta-6 desaturase, delta-6 desaturase, delta-6 desaturase, delta-6 desaturase, delta-6 desaturase, delta-6 desaturase, delta-6 desaturase, delta-6 desaturase, delta-6 desaturase, delta-6 desaturase, delta-6 desaturase, delta-6 desaturase, delta-6 desaturase, delta-6 desaturase, delta-6 desaturase, delta-6 desaturase, delta-6 desaturase, delta-6 desaturase, delta-6 desaturase, delta-6 desaturase, delta-6 desaturase, delta-6 desaturase, delta-6 desaturase, delta-6 desaturase, delta
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                          GATCCAATTTCACTATATAAATTGTGACGAAAGCAAAATGAATTCACATAGCTGAGAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel oilseed plant useful for mature seeds in which total seed fatty acid. acid profile comprises high polyunsaturated fatty acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                   oilseed plant, mature seed, seed fatty acid profile;
polyunsaturated fatty acid, oil, food, food product, beverage,
infant formula; nutritional supplement; pet food; animal feed;
whole bean soy product; aquaculture food product; soybean; annexin;
                                                                                                                                                                                                                                                                                                                                                                                           Soybean annexin promoter nucleotide sequence SEQ ID NO:3
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                                                                                       AAAGGAAAGGTTAACTAAGAAGCAATACTTCA 2012
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profile comprises polyunsaturated fatty acids. (IV) is useful for producing an oilseed plant having an altered fatty acid profile which involves transforming a plant with (IV), growing the transformed plant and selecting those plants, where the total fatty acid profile comprises 1% or more of one or more polyunsaturated fatty acid having 20 or more carbon atoms and 5 or more carbon carbon double bonds. (I) enables the production of very long chain body unsaturated fatty acids. The present sequence represents a soybean annexin promoter nucleotide sequence, which is used in the exemplification of the present invention.
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                                                                                                                                                                                             Gaps
                                                                                                                                                               100.0%; Score 2012; DB 13; Length 2012; 100.0%; Pred. No. 3.5e-225; tive 0; Mismatches 0; Indels 0;
                                                                                                                                       Sequence 2012 BP; 695 A; 326 C; 213 G; 778 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                            AATCACTCTATTTATAAATGGCATAAGGTAGTGTGGAACAATTGCAAAGCT
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Matches 2012; Conservative
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The invention relates to an isolated nucleic acid fragment comprising a seed-specific soybean annexin promoter or seed-specific soybean P34 promoter. The invention also relates to a recombinant expression construct comprising at least one heterologous nucleic acid fragment construct comprising the recombinant expression construct in its genome and a method of regulating expression of at least one heterologous nucleotide sequence in the plant. The plants are dicotyledonous plants, preferably soybean. The method of regulating expression of at least one heterologous nucleotide sequence in a plant comprises transforming a plant cell with the recombinant expression construct, growing fertile mature plants from a transformed plant cell and selecting plants comprising a transformed construct, growing fertile mature plants from a transformed plant cell and selecting plants comprising a transformed construct. Alternatively, plants comprising a transformed blant cell expressing the heterologous nucleotide sequence during early seed development are selected. The nucleic acid is useful as a plant promoter, e.g. annexin and P34 promoters. The promoters are useful in regulating or promoting expression of at least one heterologous nucleic acid fragment in plants. This sequence represents a soybean annexin promoter truncated form of the
    GATCCAATTTCACTATATAAATTGTGACGAAAGCAAAATGAATTCACATAGCTGAGAGAG 1980
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated nucleic acids comprising seed-specific soybean annexin P34 soybean promoters, useful for regulating expression of at least heterologous nucleic acid fragment in plants.
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                                                                                                                                                                                                                                                                                                                                                                           Soybean; annexin promoter; ds; dicotyledonous plant; plant
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ilarity 100.0%; Pred. No. 3.2e-210;
Conservative 0; Mismatches 0;
                                                 2012
                                                                                        2012
                                                                                                                                                                                                                                                                                                                                Soybean annexin promoter truncated sequence #1.
                                                                          AAAGGAAAGGTTAACTAAGAAGCAATACTTCA
                                                 AAAGGAAAGGTTAACTAAGAAGCAATACTTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 2; SEQ ID NO 13; 27pp; English.
                                                                                                                                                                                                    ВР
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190 ACTCTCAAGCTTTGTTTTTCGCTTCGACTCTCATGATTTCCTTCATATGCCAATCACTCT 249	ATTTATAAATGGCATAAGGTAGTGTGAACAATGCAAAGCTTGTCATCAAAAGCTTGCAA	TGTACAAATTAATGTTTTTCATGCCTTTTACAAATTATCTGCACCCCCTGCTATTAATCT	AACATCTAAGTAAGGCTAGTGAATTTTTTCGAATAGCCATGCAGTGCATTAATTTCCCCC	TGACTATTTTGGCTTTGACTCCAACACTGGCCCCGTACATCCGTCCTCATTACATGAAA	AGTTA	ATTATTATATATTACTITTTTCTCTATTCTATTACTTCTATTTTCAAATTATTATTTGCA	TATGTAAAGTACATTATATTTTTGCTATATACTTAAATATTTCTAAATTATTAAAAAAG 	ACTGATATGAAAAATTTATTCTTTTTAAAGCTATATCATTTTATATATA		AAITHAFAAAAATATTTACTTTATATGTTTTTCACATTTTTGTTAAACAATCATATC 	attatgattgaaagaggaaattgacagtgagtaataagtgatgagaaaaaaatgtgtt 	910 ATTTCCTAAAAAAACCTAAACAAACATGTATCTACTCTTATTTCATCTGTATT 969 	970 TCATTTTTCTCTTTATCTCTTTTTTTTTTTTTTTTCTATTTCACATTAATTATT	1030 TTACTCTCTTTATTTTTCTCTCTCTCTCTTATTTCCACTCATATATACACTCCAA 1089 	1090 AATTGGGGCATGCCTTTATCACTACTCTATCTCCTCCACTAAATCATTAAATGAAACTG 1149	AAAAGCATTGGCAAGTCTCCTCCCTCCTCAAGTTTTCCAACTTTGGGCATTGTGAAAAGCATTTGGAAGTTTTGGAAGTTTTGGAAGTTTTGGAAGTTTTGGAAGTTTTGGAAGTTTTGGAAGTTTTGGAAGTTTTGGAAGTTTTGGAAGTTTTGGAAGTTTTGGAAGTTTTGGAAGTTTTGGAAGTTTTGGAAGTTTTGGAAGTTTTGGAAGTTTTGGAAGTTTTGGAAGTTTTGGAAGTTTTGGAAGTTTTGGAAGTTTTGGAAGTTTTGGAAGTTTTGGAAGTTTTGGAAGTTTTGGAAGTTTTGGAAGTTTTGGAAGTTTTGGAAGTTTTGGAAGTTTTGGAAGTTTTGGAAGTTTTGGAAGTTTTGGAAGTTTTGGAAGTTTTGGAAGTTTTGGAAGTTTTGGAAGTTTTGGAAGTTTTGGAAGTTTTGGAAGTTTTGGAAGTTTTGGAAGTTTTGGAAGTTTTTGGAAGTTTTTGGAAGTTTTTGGAAGTTTTTGGAAGTTTTTT	1021 AAAAGCATTGGCAAGTCTCCTCCCTCCTCAAGTGATTTCCAACCAGCATTGGCATCTG 1080	1210 ATTGATTCAGTATATCTATTGCATGTGTAAAAGTCTTTCCACAATACATAACTTAATT 1269 1081 ATTGATTCAGTATAATTCTATTGCATGTGTAAAAGTCTTTCCACAATACATAACTTAATT 1169 1081 ATTGATTCAGTATATATCTAATGTGTAAAGTCTTTACAATAATAATAATAATAATAATAATAATAATAAT	aatcttaaataaataaaggataaaatatttttttttttt	

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                                                                                                                              New isolated nucleic acids comprising seed-specific soybean annexin and P34 soybean promoters, useful for regulating expression of at least one heterologous nucleic acid fragment in plants.
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100.0%; Pred. No. 3.4e-191;
ive 0; Mismatches 0; Indels 0;
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                                                                                                                            New isolated nucleic acids comprising
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 KINNEY A J.
LIU Z.
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The invention relates to an isolated nucleic acid fragment comprising a seed-specific soybean annexin promoter or seed-specific soybean P34 construct comprising at least one heterologous nucleic acid fragment construct comprising at least one heterologous nucleic acid fragment operably linked to any one of the isolated nucleic acid fragment a plant comprising the recombinant expression construct in its genome and a method of regulating expression of at least one heterologous nucleotide sequence in the plant. The plants are dicotyledonous plants, preferably soybean. The method of regulating expression of at least one heterologous nucleotide sequence in a plant comprises transforming a plant cell with the recombinant expression construct, growing fertile mature plants from a transformed plant cell and selecting plants comprising a transformed construct, growing fertile mature plants from a transformed plant cell expressing the heterologous nucleotide sequence during acrive delegance are useful in regulating or promoting expression of at least one heterologous nucleic acid is useful as a plant promoter, e.g. annexin and P34 promoters. The promoters are useful in regulating or promoting expression of at least one heterologous nucleic acid fragment in plants.

This sequence represents a soybean annexin promoter truncated form of the
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                                  CTCCAAAGATCCAATTTCACTATATAAATTGTGACGAAAGCAAAATGAATTCACATAGCT
                                                             CTCCAAAGATCCAATTTCACTATATAAAATTGTGAAAAGCAAAATGAATTCACATAGCT
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a plant comprising the recombinant expression construct in its genome and a method of regulating expression of at least one heterologous nucleotide sequence in the plant. The plants are dicotyledonous plants, preferably soybean. The method of regulating expression of at least one heterologous nucleotide sequence in a plant comprises transforming a plant cell with the recombinant expression construct, growing fertile mature plants from a transformed plant cell and selecting plants comprising a transformed plant cell expressing the heterologous nucleotide sequence.

Alternatively, plants comprising a transformed plant cell expressing the heterologous nucleotide sequence during early seed development are selected. The nucleic acid is useful as a plant promoter, e.g. annexin and P34 promoters. The promoters are useful in regulating or promoting expression of at least one heterologous nucleic acid fragment in plants.

This sequence represents a soybean annexin promoter truncated form of the invention.
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                                  TATATAGGTTGTACACATAATTTTATAAGGATAAAAATATGATAAAAATAAAATTTTAAA
                                                                                                                                                                                                  TTTTTTTCACATGATTTATTAACGTGCCAAAAGATGCTTATTGAATAGAGTGCACATT
                                                                                                                                                                                                                               GGCGTTAACTCCAAAGATCCAATTTCACTATATAAATTGTGACGAAAGCAAATGAATTC
                                                                 TACAACCTTAGTAATTCATAAATTCCTATATGTATATTTGAAATTAAAAACAGATAATCG
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                                                                                                              CGAAAAACCACCTCACCATGAATCACTCTTCACACCATTTTTACTAGCAAACAAGTCTCA
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                                                                                                                                                           TITITITICACATGATTTATTAACGTGCCAAAAGATGCTTATTGAATAGAGTGCACATT
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The invention relates to an isolated nucleic acid fragment comprising a seed-specific soybean annexin promoter or seed-specific soybean P34 comprising at least one heterologous nucleic acid fragment construct comprising at least one heterologous nucleic acid fragment operably linked to any one of the isolated nucleic acid fragment above, a plant comprising the recombinant expression construct in its genome and a method of regulating expression of at least one heterologous nucleotide sequence in the plant. The plants are dicotyledonous plants, preferably soybean. The method of regulating expression of at least one heterologous nucleotide sequence in a plant comprises transforming a plant cell with the recombinant expression construct, growing fertile mature plants from a transformed plant cell and selecting plants comprising a transformed construct, growing fertile mature plants from a transformed plant cell and selecting plants comprising a transformed construct, growing fertile mature plants from a transformed plant cell expressing the heterologous nucleotide sequence during early seed development are construct, and plant promoter, e.g. annexin and plant promoters. The promoters are useful in regulating or promoting expression of at least one heterologous nucleic acid fragment in plants. This sequence represents a soybean annexin promoter truncated form of the construct.
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100.0%; Pred. No. 2.5e-126;
ive 0; Mismatches 0;
heterologous nucleic acid fragment in plants.
                                                           Claim 2; SEQ ID NO 17; 27pp; English.
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and
                                                              CTTCACACCATTTTTACTAGCAAACAAGTCTCAACTGAAGCCAGCTCTCTTTCCGTT
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                 TATITIAGCCATAAATAAATGACCAGCATATITIACAACCTTAGTAATTCATAAATTCCT
                                                                                       TTGCCATTTGTTTTTCATGCAAACAGAAAGGGACGAAAAACCACCTCACCATGAATCACT
                                                                                                                         CTTCACACCATTTTTACTAGCAAACAAGTCTCAACAACTGAAGCCAGCTCTTTCCGTT
                                                                                                                                                            TATITIAGCCATAAATAAATGACCAGCATATITIACAACCTTAGTAATICATAAATICCT
                                                    New isolated nucleic acids comprising seed-specific soybean annexin P34 soybean promoters, useful for regulating expression of at least heterologous nucleic acid fragment in plants.
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                                                                                                                                                                                                                                                                                                                                                                                                                      Soybean annexin promoter truncated sequence #6.
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The invention relates to an isolated nucleic acid fragment comprising a seed-specific soybean annexin promoter or seed-specific soybean P34 construct comprising at least one heterologous nucleic acid fragment construct comprising at least one heterologous nucleic acid fragment operably linked to any one of the isolated nucleic acid fragments above, a plant comprising the recombinant expression construct in its genome and a method of regulating expression of at least one heterologous nucleotide sequence in the plant. The plants are dicotyledonous plants, preferably soybean. The method of regulating expression of at least one heterologous nucleotide sequence in a plant comprises transforming a plant cell with the recombinant expression construct, growing fertile mature plants from a transformed plant cell and selecting plants comprising a transformed to the recombinant expression construct, growing fertile mature plants from a transformed plant cell and selecting plants comprising a transformed construct. Growing fertile expressing the heterologous nucleotide sequence during early seed development are construct. The nucleic acid is useful as a plant promoter, e.g. annexin and P34 promoters. The promoters are useful in regulating or promoting expression of at least one heterologous nucleic acid fragment in plants. This sequence represents a soybean annexin promoter truncated form of the
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48.1%; Score 967; DB 13; Length 967;
Best Local Similarity 100.0%; Pred. No. 6.2e-104;
Matches 967; Conservative 0; Mismatches 0; Indels (
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Best Local Similarity
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AATAAATGACCAGCATATTTTACAACCTTAGTAATTCATAAATTCCTATATGTATATTTG **AAATTAAAAACAGATAATCGTTAAGGGAAGGAATCCTACGTCATCTCTTGCCATTTGTTT** AAATTAAAAACAGATAATCGTTAAGGGAAGGAATCCTACGTCATCTTGCTTTGTTT TTCATGCAAACAGAAAGGGACGAAAAAACCACCTCACCATGAATCACTCTTCACACCATTT TTCATGCAAACAGAAAAGCGACGACCTCACCATGAATCACTCTTCACACTTT

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18-NOV-2004
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Alternatively, plants comprising a transformed plant cell expressing the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated nucleic acids comprising seed-specific soybean annexin and P34 soybean promoters, useful for regulating expression of at least one heterologous nucleic acid fragment in plants.
GACGAAAGCAAAATGAATTCACATAGCTGAGAGAAAAGGAAAAGGTTAACTAAGAAA
                                                CTTTCTTTGAAATAGTAGTATTTTTTTTTTCACATGATTTATTAATAACGTGCCCAAAAGATGCT
                                                                                  TATTGAATAGAGTGCACATTTGTAATGTACTACTAATTAGAACATGAAAAAGCATTGTTC
                                                                                             TAACACGATAATCCTGTGAAGGCGTTAACTCCAAAGATCCAATTTCACTATATAAATTGT
                                                                                                                                              TAACACGATAATCCTGTGAAGGCGTTAACTCCCAAAGATCCAATTTCACTATATAAATTGT
                                                                                                                                                                                GACGAAAGCAAAATGAATTCACATAGCTGAGAGAGAAAGGAAAGGTTAACTAAGAAGCAA
                                    CTTTCTTTGAAATAGTAGTATTTTTTTTCACATGATTTATTAACGTGCCAAAAGATGCT
                                                                                                                                                                                                                                                                                                                                                                                                              Soybean; annexin promoter; ds; dicotyledonous plant; plant
                                                                                                                                                                                                                                                                                                                                                                                         Soybean annexin promoter truncated sequence #7
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LIU Z.
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heterologous nucleotide sequence during early seed development are selected. The nucleic acid is useful as a plant promoter, e.g. annexin and P34 promoters. The promoters are useful in regulating or promoting expression of at least one heterologous nucleic acid fragment in plants. This sequence represents a soybean annexin promoter truncated form of the invention.
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                                                                                                                                                Sequence 770 BP; 303 A; 108 C; 89 G; 270 T; 0 U; 0 Other;
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100.0%; Pred. No. 4.5e-81;
rive 0; Mismatches 0;
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Matches 770; Conservative
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Best Local S
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The invention relates to an isolated nucleic acid fragment comprising a seed-specific soybean annexin promoter or seed-specific soybean P34 procession also relates to a recombinant expression construct comprising at least one heterologous nucleic acid fragment operably linked to any one of the isolated nucleic acid fragments above, a plant comprising the recombinant expression construct in its genome and a method of regulating expression of least one heterologous nucleotide sequence in the plant. The plants are dicotyledonous plants, preferably soybean. The method of regulating expression of at least one heterologous construct, growing fertile mature plants from the recombinant expression construct, growing fertile mature plants from a transformed plant cell and selecting plants comprising a transformed a lateratively, plants comprising a transformed a lateratively, plants comprising a transformed a lateratively, plants comprising a transformed heterologous nucleotide sequence during early seed development are
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241 AAAACCACCTCACCATGAATCACTCTTCACACCATTTTTACTAGCAAACAAGTCTCAACA 300
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                                                                                            TITITICACATGATITATTAACGIGCCAAAAGAIGCTIATIGAATAGAGIGCACATITGI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 584; DB 13;
Pred. No. 1.8e-59;
                         Soybean annexin promoter truncated sequence #8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 2; SEQ ID NO 20; 27pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29.0%; Sco
llarity 100.0%; Pr
Conservative 0;
                                                                                                                                                                                                                                                                  11-FEB-2004; 2004US-00776889
                                                                                                                                                                                                                                                                                                               12-FEB-2003; 2003US-0446833P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2004-592806/57.
                                                                                                                                                                                                                                                                                                                                                            (KINN/) KINNEY A J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Kinney AJ, Liu Z;
                                                                                                                                                                  JS2004158052-A1
                                                                                                                                                                                                                                                                                                                                                                                     (LIUZ/) LIU Z.
                                                                                                                                                                                                                  12-AUG-2004.
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                                                                                                                     Glycine
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selected. The nucleic acid is useful as a plant promoter, e.g. annexin and P34 promoters. The promoters are useful in regulating or promoting expression of at least one heterologous nucleic acid fragment in plants. This sequence represents a soybean annexin promoter truncated form of th
                                                                                                                                                               CATGCAAACAGAAAAGGGACGAAAAACCACCTCACCATGAATCACTCTCACACCACCATTTTT
                                                                                                                                                                                                     TTCTTTGAAATAGTAGTATTTTTTTTTCACATGATTTATTAACGTGCCAAAAGATGCTTA
                                                                                                                                                                                                                                                                                 TTGAATAGAGTGCACATTTGTAATGTACTACTAATTAGAACATGAAAAAGCATTGTTCTA
                                                                                                                                                                                                                                                                                                                      ACACGATAATCCTGTGAAGGCGTTAACTCCAAAGATCCAATTTCACTATATAAAATTGTGA
                                                                                                                1588 ATTAAAAACAGATAATCGTTAAGGGAAGGAATCCTACGTCATCTTCTTGCCATTTGTTTTT
                                                                                                                                  1 ATTAMAMACAGATAMTCGTTAMGGGAMGGAMTCCTACGTCATCTTGCTTTTTTT
                                                                                                                                                     1648 CATGCAAACAGAAAGGGACGAAAAACCACCTCACCATGAATCACTTCTCACCATTTTT
                                                                                                                                                                                           ACTAGCAAACAAGTCTCAACAACTGAAGCCAGCTCTCTTTCCGTTTCTTTTACAACACT
                                                                                                                                                                                                                               TTGAATAGAGTGCACATTTGTAATGTACTACTAATTAGAACATGAAAAAGCATTGTTCTA
                                                                                                                                                                                                                                                                                                          ACACGATAATCCTGTGAAGGCGTTAACTCCAAAGATCCAATTTCACTATATAAATTGTGA
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                                                                                               Gaps
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0
                                                                             Length 425;
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                                                          Sequence 425 BP; 154 A; 81 C; 64 G; 126 T; 0 U; 0 Other;
                                                                           21.1%; Score 425; DB 13;
100.0%; Pred. No. 5.1e-41;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Soybean annexin promoter truncated sequence #10
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                                                                           Query Match
Best Local Similarity 100.
Matches 425; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                      CTTCA 425
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promoter. The invention also relates to a recombinant expression construct comprising at least one heterologous nucleic acid fragment operably linked to any one of the isolated nucleic acid fragment operably linked to any one of the isolated nucleic acid fragment above, operably linked to any one of the isolated nucleic acid fragment above, a plant comprising the recombinant expression construct in its genome and a method of regulating expression of at least one heterologous nucleotide sequence in the plant. The plants are dicotyledonous plants, preferably solveson. The method of regulating expression of at least one heterologous nucleotide sequence in a plant comprises transforming a plant cell with the recombinant expression construct, growing fertile mature plants from a transformed plant cell and selecting plants comprising a transformed to the respective sequence.

Chiant cell expression construct, growing fertile expressing the heterologous nucleotide sequence.

Alternatively, plants comprising a transformed plant cell expressing the heterologous nucleic acid is useful as a plant promoter, e.g. annexin and P34 promoters. The promoters are useful in regulating or promoting expression of at least one heterologous nucleic acid fragment in plants.

Chis sequence represents a soybean annexin promoter truncated form of the
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neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;
New isolated nucleic acids comprising seed-specific soybean annexin and P34 soybean promoters, useful for regulating expression of at least one heterologous nucleic acid fragment in plants.
                                                                                                                                                                                                                                             invention relates to an isolated nucleic acid fragment comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1839 GCACATTTGTAATGTACTACTAATTAGAACATGAAAAAGCATTGTTCTAACACGATAATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 174; DB 13;
Pred. No. 7.6e-12;
0; Mismatches 0;
                                                                                                                                                              Claim 2; SEQ ID NO 22; 27pp; English
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100.0%; Pre
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Matches 174;
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Detecting and differentiating between hematopoietic cell proliferative
                                  AAGCATTGGCAAGTCTCCTCCCCTCCAAGTGATTTCCAACTCAGCATTGGCATCTGAT
                                                                1212 IGATICAGIATATCIATIGCATGIGIAAAAGICTTICCACAATACAIAACTATTAATTAA
                                                                                                                                   12361 İGİTATATATATATATATATATATATATATGTTATGTATATATATATATAT
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P, Grabs G, Lesche R, Leu E;
Model F, Mueller V, Otto T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12720 İTTATATATATATATATATATATİTÇGİATATATA 12757
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Jolek A, Piepenbrock C, Adorjan
Lewin A, Lipscher E, Maier S,
Schwope I, Ziebarth H;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8
                                                                                                                                                                                                                                                                       The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, Alzheijepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           614
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                                                                                                                                                                                       cytosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         555 TATATTACTTTTTCTCTATTCTATTAGTTCTATTTTCAAATTATTATTATGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TATTGTTTATATTCTTAATTAAAAATATTGTCCCTTCTAAATTTTTCATATAGTTAATTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                fragment of chemically modified gene, useful of diseases associated with abnormal cytosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 15548 BP; 4209 A; 247 C; 2903 G; 8189 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 15548;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7.8%; Score 156; DB 6; Length 155
50.4%; Pred. No. 4.5e-10;
ive 0; Mismatches 565; Indels
                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 2128; 32pp + Sequence Listing; German.
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                                                                                                   Berlin
              30-JUN-2000; 2000DE-01032529.
01-SEP-2000; 2000DE-01043826.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 50.4°
Matches 594; Conservative
                                                                                                                                                                     Nucleic acid comprising diagnosis and treatment
                                                                                                   ပဲ
                                                                (EPIG-) EPIGENOMICS AG
                                                                                                 Piepenbrock
                                                                                                                                     WPI; 2002-130909/17
                                                                                                                                                                                                         methylation.
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The present invention describes a method for detecting and differentiating between haematopoietic cell proliferative disorders associated with at least 1 gene and/or their regulatory regions in a subject. The method comprises contacting a target nucleic acid in a biological sample obtained from the subject with at least 1 reagent, which distinguishes between methylated and non-methylated CpG dinucleotides within the target nucleic acid. ABZ09861 to ABZ1118 represent specifically claimed nucleotide sequences from the present invention. Oligonucleotides from the present invention can be used: for differentiating between healthy haematopoietic cells and proliferative classocial calls; for differentiating between acute ilymphocytic leukaemia and acute myelogenous leukaemia; as probes for determining the cytosine methylation state and/or single nucleotide polymorphisms (SNPs) of haematopoietic cell proliferation disorder æ related sequences and their complements; and as primers for the amplification of haematopoietic cell proliferation disorder related DNA sequences. The nucleotide sequences from the present invention can also be used for detecting a predisposition to, differentiation between subclasses, diagnosis, prognosis, treatment and/or monitoring of haematopoietic cell proliferative disorders. The present method enables highly specific classification of haematopoietic cell proliferative disorders allowing for improved and informed treatment of patients disorders, comprises contacting a target nucleic acid with a reagent t distinguishes between methylated and non-methylated CpG dinucleotides. SEQ ID NO 386; 117pp; English 28; Claim

Sequence 8056 BP; 3711 A; 0 C; 371 G; 3974 T; 0 U; 0 Other;

2484 2304 2064 1947 5 2007 314 614 434 494 TITICGCTCCTATICAAATACTGTATITITACCAAAAAACTGTATT-TITICCTACACTCT 194 75 2363 AAAATTATATTTAAAAATTAAATTAAATTTÄTTTAAATACAAAAATTAATAATTATTTT 16 TTATATGGTGTTTAGATGGATTCACATGCAAGTTTTTATTTCAATCCCTTTTCCTTTGAA 2423 ATTATTTTTTTTTAÄTTTTCAAAAATAATAÄÄÄTTTÄATAAÄTTATTATAÄÄÄTAA CAAGCTTTGTTTTTCGCTTCGACTCTCATGATTTCCTTCATATGCCAATCACTCTATTTA TAAATGCCATAAGGTAGTGTGAACAATTGCAAAGCTTGTCATCAAAAGCTTGCAATGTAC AAATTAATGTTTTTCATGCCTTTCAAAATTATCTGCACCCCCTAGCTATTAATCTAACAT CTAAGTAAGGCTAGTGAATTTTTCGAATAGTCATGCAGTGCATTAATTTCCCCGTGACT TATTGTTTATATTCTTAAAAATATTGTCCCTTCTAAAATTTTCATATAGTTAATTAT TITITITAAAATAAAATAITITAAAATATATITIT---ATTITAAAATATTITAAAATT TATATTACTTTTTCTCTATTCTATTAGTTCTATTTTCAAATTATTATTATGCATATGT Gaps Indels 10; DB 8; Length 8056; tch 7.5%; Score 150.2; DB 8; al Similarity 45.5%; Pred. No. 2.3e-09; 725; Conservative 0; Mismatches 858; 2483 2123 2063 2006 Query Match 2543 92 136 195 255 315 375 435 495 Local Matches 임 ò 셤 ઠે 요 ò 임 ò g ઠે 셤 g ઠે 셤 ઠે ઠે 셤 ઠે ઠે

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1092 1272 1332 1570 1333 TTGTTTAGATGTATATTCGAATAAATCTAAATATATGATAATGATTTTTTATATTGATTA 1392 854 914 974 CITICALITITCIATICAATITAATAAGAAATAAATITITGIAAATITITATITATCAATIT 795 ATAAAAATATTTTACTTTATATGTTTTTTCACATTTTTTGTTAAACAAATCATATCATTAT GATTGAAAGAGAAATTGACAGTGAGTAATAAGTGATGAGAAAAAATGTGTTTTTTC 1646 ITITAATITIACAATICAITIATTITICAATITITIAAAAIAITAAAAITATAAATIATAAAI TITCICITITATCITITCITITITITITATCATATCATITCACATT - - AATTATTITA AGCATTGGCAAGTCTCCTCCCTCCTCAAGTGATTTCCAACTCAGCATTGGCATCTGATT 1513 TATTTTAGCCATAAATAAATGACCAGCATATTTT--ACAACCTTAGTAATTCATAAATTC 1033 CTCTCTTTATTTTTCTCTCTATCCCTCTTATTTCCACTCATATATACACTCCAAAAT TGGGGCATGCCTTTATCACTATCTCTCCTCCACTAAATCATTTAAATGAAACTGAAA CITAAATAAATAAAGGATAAAATATITITITITITICTICATAAAATTAAAATATGITATITIT aritacattritatatattatatattacataacattrittrittritatrcaaaaaritatt 1393 AACATATAAATCAATATTAAATATGATATTTTTTTTTATAGGTTGTACACATAATTTTATA CTATATGTATTTGAAATTAAAACAGATAAT 1603 TAATATATTTTTTTTTTAATAAAAAT 956 1826 975 615 855 675 735 1466 1153 1348 1273 1288 1453 1093 1168 g a g ò g ò ઠે a 셤 g 셤 윱 g ઠે ò 용 ò ò à ठ ò ò g ठे 셤 g 셤

RESULT 15 ABZ10246 ID ABZ100

ABZ10246 standard; DNA; 8056

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610 TATGTAAAGTACATTATATTTTTGCTATATACTTAAATATTTCTAAATTATTAAAAAAG
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Job time : 787.833 secs
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                                                                            Haematopoietic cell proliferation disorder related DNA sequence #386
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                                                                                                                           gene therapy, lymphocytic leukaemia, acute myelogenous leukaemia, cytosine methylation state, gene; ds.
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P, Grabs G, Lesche R, Leu E;
Model F, Mueller V, Otto T, I
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                                                                                                          Human, haematopoietic cell proliferation disorder,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 28; SEQ ID NO 386; 117pp; English.
                                                                                                                                                                                                                                                                                                                                                                    Berlin K, Braun A, Distler J,
Olek A, Piepenbrock C, Adorjan
Lewin A, Lipscher E, Maier S,
Schwope I, Ziebarth H,
                                                                                                                                                                                                                                                                         26-MAR-2002; 2002WO-EP003401
                                                                                                                                                                                                                                                                                                        26-MAR-2001; 2001US-0278333P.
                                              (first entry)
                                                                                                                                                                                                                                                                                                                                      (EPIG-) EPIGENOMICS AG.
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Olek A, P
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                                                     ACTGATATGAAAAATTTATTCTTTTAAAGCTATATCATTTTATATACTTTTTCTTTT
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CH261-180 ip15c02.b P041-2-A0 Mus muscu CH261-167

Мив шивси

ISB1-1230 CH216-130

CH216-151

CH216-143 Мив шивси

CL062848 CCG74848 CCG74848 CCC253231 CCC253231 CCC253231 CCG7476149 CCG7476149 CCG771210 CCG771210 CCG771210 CCG771210 CCG771210 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189 ACG76189

Mus muscu CH216-151

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Tetraodon Arabidops ENTDP49TF

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ALIGNMENTS

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S. Xenopus tropicalis (western clawed frog)

Xenopus tropicalis (western clawed frog)

Eukaryota, Metazod; Chordata, Craniata; Vertebrata; Euteleostomi,

Amphibia, Batrachia, Amura; Mesobatrachia; Pipoidea; Pipidae;

Xenopodinae; Xenopus; Silurana.

El (Bases I to 1626)

B. (Bases I to 1626)

A. Unpublished (1999)

Contact: Daniela S. Gerhard, Ph.D.

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: cgapbs-remail.ini.gov

Tissue Procurement: Robert M. Grainger

cDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

cDNA Library Preparation: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image:llnl.gov

Plate: LLAMA4680 row: g column: 21

High quality sequence stop: 316.

Location/Qualifiers

Location/Qualifiers
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AGENCOURT 15099447 NICHD XGC Emb6 Xenopus tropicalis cDNA clone
IMAGE:6995950 5', mRNA sequence.
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/dev stages="mbryo, stages 14-19"
/dev stages="mbryo, stages 14-19"
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/note="Vector: pCMV-SPORT6 1; Site 1: NotI; Site 2: EcoRV;
Cloned unidirectionally. Primer: Oligo dT. Average insert size 2.1 kb. Constructed by Invitrogen. Note: This is a Xenopus Gene Collection (XGC) library."

    .1626
    /organism="Xenopus tropicalis"

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/db_xref="taxon:8364"
/clone="IMAGE:6995950"
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CC253231
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CG7550B P048-1-C0
AG350209 Mus muscu
CG74972B P044-1-C0
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CL082569 CH216-167
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1348 bp DNA linear GSS 24-OCT-2003
P043-4-A06.za Ppa EcoRI BAC Library Pristionchus pacificus genomic,
genomic survey sequence.
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Neodiplogasteridae; Pristionchus.
1 (bases I to 1348)
Srinivasan, J., Sinz, W., Jesse, T., Wiggers-Perebolte, L., Jansen, K.,
Buntjer, J., van der Meulen, M. and Sommer, R.J.
An integrated physical and genetic map of the nematode Pristionchus
1513 TATTTTAGCCATAAATAAATGACCAGCATATTTTACAACCTTAGTAATTCATAAATTCCT 1572
                                                                  465 TACATCCGTCCCTCATTACATGAAAAGAAATATTGTTTATATTTAAAAATATTG 524
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Max-Planck-Institute for Developmental Biology
Spemanistr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
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/strain="California"
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45.8%; Pred. No. 2e-14;
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          TAAGAAATAAATTTTTGTAAATTTTTATTTATCAATTTTATAAAAATATTTTACTTTATATG
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1608 bp DNA linear GSS 05-JAN-2004
ISB1-72J8_T7.1 ISB1 Xenopus tropicalis genomic clone ISB1-72J8,
GENOMIC Burvey sequence.
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GESS
                                                                                                                         Xenopus tropicalis (western clawed frog)
Kenopus tropicalis
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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VERSION KEYWORDS SOURCE ORGANISM

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                1 (bases 1 to 1608)

Kremitzki,C., Carter,J., McPherson,J., Warren,W., Graves,T., Mardis,E. and Wilson,R.
A physical map of the xenopus tropicalis genome
Unpublished (2003)
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/organism="Xenopus tropicalis"
/organism="Xenopus DNA"
/ob_xref="taxon:8364"
/clone="ISB1-72J8"
/clone="ISB1-72J8"
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Genome Sequencing Center
Washington University School of Medicine
Washington University School of Medicine
Insert Length: 75000
Seq primer: T7 TAATACGACTCACTATAGGG
Class: BAC ends
High quality sequence start: 252
High quality sequence stop: 345.
Location/Qualifiers
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Pred. No. 1.1e-12;
0; Mismatches 522;
Kenopodinae; Xenopus; Silurana
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           1140 AATGAAACTGAAAAGCATTGGCAAGTCTCCTCCCCTCCTCAAGTGATTTCCAACTCAGCA 1199
                                                      TTGGCATCTGATTGATTCAGTATATCTATTGCATGTGTAAAAGTCTTTCCACAATACATA 1259
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                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopus; Silurana.

1 (bases 1 to 1242)
Kremitzki,C., Carter,J., McPherson,J., Warren,W., Graves,T., Aphysical map of the xenopus tropicalis genome
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tropicalis
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Pred. No. 1.4e-12;
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/clone_lib="CH216"
/note="Vector: pTARBAC2.1; CHORI-216 Xenopus
ACC_library"
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Washington University School of Medicine
Email: submissions@watson.wustl.edu
Insert Length: 175000 Std Error: 0.00
Seq primer: Sp6 ATTTAGGTGACACTATAG
Class: BAC ends
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mol_type="genomic DNA"
fstrain="Nigerian frog"
db_xref="taxon:8364"
clone="CH216-115B3"
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High quality sequence stop: 57.
Location/Qualifiers
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S Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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BAC end Sequences of Library MSMg01
Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /sex="male"
/tissue_type="mixture of kidney and spleen"
/clone_lib="MSMg01 Mouse Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Mus musculus molossinus"
/mol_type="genomic DNA"
/mul_type="genomic DNA"
/mul_type="molossinus"
/db_xref="taxon:57486"
/clone="MSMg01-201G10.TJ"
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Location/Qualifiers
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Mus musculus molossinus
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P048-1-C01.za Ppa EcoRI BAC Library Pristionchus pacificus genomic,
genomic survey sequence.
CG753083
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Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
1 (bases 1 to 1896)
Srinivasan, J., Sinz, W., Jesse, T., Wiggers-Perebolte, L., Jansen, K., Buntjer, J., van der Meulen, M. and Sommer, R.J.
An integrated physical and genetic map of the nematode Pristionchus pacificus
Mol. Genet. Genomics 269 (5), 715-722 (2003)
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Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
Direct Submission

Light State (17-Nov-2013) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suchiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:hattoriogec.riken.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-803-9111, Fax:81-45-503-9170)

Clones are derived from the mouse BAC library MSMg01. For BAC library availability, please contact Kuniya Abe (abe@rtc.riken.jp). Tsukuba Institute of Physical and Chemical Research (RIKEN) 3-1-1

Koyadai, Tsukuba, 305-0074 Japan

phone: 81-298-36-9189, fax: 81-298-36-9199
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                   CATTGGCATCTGATTGATTCAGTATATCTATTGCATGTGTAAAAGTCTTTCCACAATACA 1257
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Mus musculus molossinus DNA, clone:MSMg01-146M02.TJ, genomic survey
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                       Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
BAC end Sequences of Library MSMg01
Unpublished
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                                                                                                                                                                                                                                                          /db xref="taxon:54126"
/clone lib="Ppa EcoRI BAC Library"
/note="The library was generated by a partial digest the genomic DNA with EcoRI and cloning into the BAC vector."
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                                                                                                                                                                                                                                                                                                                                                                                                                          24;
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Pred. No. 3.9e-12;
0; Mismatches 584; Indels
                                             Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
                                                                                                                                                                                                     /organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
                                                                                                                      Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
Class: BAC ends.
                                                                                                                                                                          Location/Qualifiers
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Best Local Similarity
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                                                                                DB 9; Length 1378;
                                                /tissue_type="mixture of kidney and spleen"
/clone_lib="MSMg01 Mouse Male BAC Library"
                                                                                 Score 155.4; DB 9; Length:
Pred. No. 4.6e-12;
0; Mismatches 532; Indels
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       /mol_type="genomic DNA"
/mub species="molossinus"
/db xref="taxon:57486"
/clone="MSWg01-146M02.TJ"
/sex="male"
                                                                                Query Match
Best Local Similarity 49.6%;
Matches 544; Conservative (
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Eukaryota; Mefazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
1. (bases 1 to 1210)
Srinivasan, J., Sinz,
Buntjer,J., van der Meulen,M. and Sommer,R.J.
An integrated physical and genetic map of the nematode Pristionchus 1508 AAAAATATTTTAGCCATAAATAAATGACCAGCATATTTTACAACCTTAGTAATTCATAAA 1567 CG749728 P044-1-C03.za Ppa EcoRI BAC Library Pristionchus pacificus genomic, ä TATTGTTTATATTCTTAATATTATTGTCCCTTCTAAATTTTCATATAGTTATAT 554 TATATTACTTTTTCTCTATTAGTTCTATTTTCAAATTATTATTATTATGCATATGT 614 ō 1452 AAGGATAAAAATATGATAAAATAAATTTTA----AATATTTTATATTTACGAGAAAA <u>AAACATATAATCAATATTAAATATGATATTTTTTTTTATATGGTTGTACACATAATTTTAT</u> /db_xrefe"taxon:54126" /clone lib="Ppa EcoRI BAC Library" /note="The library was generated by a partial digest the genomic DNA with EcoRI and cloning into the BAC vector." Gaps 12; Length 1210; Indela Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemanustr. 37-39, Tuebingen D-72076, Germany
Tat: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de pacificus Mol. Genet. Genomics 269 (5), 715-722 (2003) 22835951 /organism="Pristionchus pacificus" /mol_type="genomic DNA" /strain="California" Query Match 7.7%; Score 154.4; DB 9; Best Local Similarity 46.1%; Pred. No. 6.5e-12; Matches 463; Conservative 0; Mismatches 529; Location/Qualifiers genomic survey sequence. CG749728 1568 TICCIATATGTATAT 1583 1353 ATAATATAATTAAATT 1368 CG749728.1 GI:37970654 Pristionchus pacificus Pristionchus pacificus

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/clone lib="CH216"
/note="Vector: pTARBAC2.1; CHORI-216 Xenopus tropicalis
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Pred. No. 9.5e-12;
0; Mismatches 687; Indels
              A physical map of the xenopus tropicalis genome Unpublished (2003)
Contact: Richard K Wilson
                                                           Genome Sequencing Center
Mashington University School of Medicine
Email: submissions@watson.wustl.edu
Insert Length: 175000 Std Brror: 0.00
Seq primer: RM4 ctcaagggcatcggtcgagc
Class: BAC ends
High quality sequence start: 690
High quality sequence start: 690
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/organism="Xenopus tropicalis"
/mol type="genomic DNA"
/strain="Nigerian frog"
/db xref="caxon:8864"
/clone="CH16-15918"
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Mardis, E. and Wilson, R.
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Matches 623, Conservative
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Amopodinae; Xenopus; Silurana.
1 (bases 1 to 1805)
Kremitzki,C., Carter,J., McPherson,J., Warren,W., Graves,T.,
                                                                                                                 507 NTINITITITITITITITITITITAAAATIATITAATGIAAANIAAAGAATIAITIA
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Spemannstr. 37-39, Tuebingen D-72
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.class: BAC ends.
Location/Qualifiers
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Best Local Similarity 48.7%;
Matches 535; Conservative
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P052-4-C08.za Ppa EcoRI BAC Library Pristionchus pacificus genomic,
genomic survey sequence.
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Srinivasan,J., Sinz,W., Jesse,T., Wiggers-Perebolte,L., Jansen,K.,
Buntjer,J., van der Meulen,M. and Sommer,R.J.
An integrated physical and genetic map of the nematode Pristionchus
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                                   TAAATAAATAAAGGATAAATATTTTTTTTTTTCTTCATAAAATTAAAATATGTTATTTTT
                                                                                                                                 GTTTAGATGTATATTCGAATAAATCTAAATATATATGATAATGATTTTTTATATTGATTAAA
                                                                                                                                                                                CATATAATCAATATTAAATATGATATTTTTTTTATATAGGTTGTACACATAATTTTTATAAG
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Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridas; Pristionchus.
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Evolutionary Biology
Max-Planck-Institute for Developmental Biology
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CG757503.1 GI:37986131
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/clone_lib="Ppa EcoRI BAC Library"
/note="The library was generated by a partial digest
the genomic DNA with EcoRI and cloning into the BAC
vector."
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Pred. No. 1.1e-11;
0; Mismatches 550;
Tuebingen D-72076,
                                                                                               1. .1392
/organism="Pristionchus
/mol_type="genomic DNA"
/strain="California"
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CL110653 1594 bp DNA linear GSS 05-JAN-2004 ISB1-53P23_Sp6.1 ISB1 Kenopus tropicalis genomic clone ISB1-53P23, genomic survey sequence. CL110653.1 GI:40604288
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                                       615 AAAGTACATTATATTTTGCTATATACTTAAATATTTCTAAATTATTAAAAAAAGACTGA
                                                                                              795 ATAAAAATATTTTACTTTATATGTTTTTTCACATTTTTGTTAAACAAATCATATCATTAT
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                                                     TGTTTAGATGTATATTCGAATAAATCTAAATATATGATAATGATTTTTTATATTGATTAA 1393
                                                                                 ATTTTAGCCATAAATAAATGACCAGCATATTTTACAACCTTAGTAATTCATAAATTCCTA 1573
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Xenopus tropicalis (western clawed frog)

Xenopus tropicalis

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Amphibia; Batracotia; Anura; Mesobatrachia; Pipoidea; Pipidae;

Xenopodinae; Xenopus; Silurana.

1 (bases 1 to 1632)

Kremitzki,C., Carter,J., McPherson,J., Warren,W., Graves,T.,

Mardis,E. and Wilson,R.

A physical map of the xenopus tropicalis genome
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /sex="male"
/cell_line="Stock 248 F7A2, inbred N7"
/clone_line="CH216"
/note="Vector: pTARBAC2.1; CHORI-216 Xenopus tropicalis
BAC library"
                                                                                                                                         ACATATAATCAATATTAAATATGATATTTTTTTATATAGGTTGTACACATAATTTTATAA
                                                                                                                                                                     GGATAAAAATTTTAAAATTTTTAAATTTTTAAATATTTTACGAGAAAAAAA
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Pred. No. 1.2e-11;
0; Mismatches 525; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Richard K Wilson
Genome Sequencing Center
Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: submissions@watson.wustl.edu
Insert Length: 175000 Std Error: 0.00
Seq primer: Sp6 ATTTAGGTGACACTATAG
Class: BAC
High quality sequence start: 1062
High quality sequence stop: 1114.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Xenopus tropicalis"
/mol_type="genomic DNA"
/strain="Nigerian frog"
/db_xref="taxon:8364"
/clone="CH216-167P5"
                                                                                                                                                                                                                                                                                    TATGTATATTTGAAATTAA 1592
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ilarity 47.2%;
Conservative
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1594 bp DNA linear GSS 31-DEC-2003 CHILG-4646_Sp6.1 CH216 Xenopus tropicalis genomic clone CH216-46A6, CL038406
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/clone lib="CH216"
/note="Vector: pTARBAC2.1; CHORI-216 Xenopus tropicalis
BAC library"
                                       1095 GGGCATGCCTTTATCACTACTCTTCTCCTCCACTAAATCAATGAAACTGAAAAG
                                                                             1155 CATTGGCAAGTCTCCTCCCTCCTCAAGTGATTTCCAACTCAGCATTGGCATCTGATTGA
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                                                                                                                                                                                                                                                                                                        Xenopus tropicalis (western clawed frog)

Xenopus tropicalis

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostc

Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;

Xenopodinae; Xenopus; Silurana.

1 (bases 1 to 1594)

Kremitaki,C., Carter,J., McPherson,J., Warren,W., Graves,T.,

Mardis,E. and Wilson,R.

A physical map of the xenopus tropicalis genome

Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7.5%; Score 150.6; DB 9; Length 1594;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genome Sequencing Center
Washington University School of Medicine
Email: submissions@watson.wustl.edu
Insert Length: 175000 Std Error: 0.00
Seq primer: Sp6 ATTTAGGTGACACTATAG
Class: BAC ends
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High quality sequence stop: 522.
Location/Qualifiers
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/db_xref="taxon:8364"
/clone="CH216-46A6"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CL038406.1 GI:40494319
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           Xenopus tropicalis (western clawed frog)

Xenopus tropicalis

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;

Xenopodinae; Xenopus; Silurana.

(Kremizzki,C., Carter,J., McPherson,J., Warren,W., Graves,T.,

Mardis,E. and Wilson,R.

A physical map of the xenopus tropicalis genome

Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clome="1SB1-53P23"
/clome lib="1SB1"
/note="Vector: pBeloBAC11; ISB-1 Xenopus tropicalis BAC
Library Segment 1"
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47.7%; Pred. No. 1.3e-11;
iive 0; Mismatches 520; Indels
                                                                                                                                                                                                     Contact: Richard K Wilson
Genome Sequencing Center
Washington University School of Medicine
Email: submissions@watson.wustl.edu
Insert Length: 75000 Std. Error: 0.00
Seq primer: Sp6 ATTAGGTGACACTATAG
Class: BAC ends
High quality sequence start: 390
High quality sequence stop: 470.
                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Xenopus tropicalis"
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/db_xref="taxon:8364"
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Matches 479; Conservative
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CH216-165P18_RM4.1 CH216 Xenopus tropicalis genomic clone CH216-165P18, genomic survey sequence.
CL082000
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1. (Dases I to 1981)

Kremitzki, C., Carter, J., McPherson, J., Warren, W., Graves, T., Mardis, E. and Wilson, R.

A physical map of the xenopus tropicalis genome
Unpublished (2003)

Contact: Richard K Wilson
                                                                                                                                                                                                                                                                                                                                                                                                                           /cell_line="Stock 248 F7A2, inbred N7"
/clone_lib="CH216"
/note="Vector: pTARBAC2.1; CHORI-216 Xenopus tropicalis
BAC library"
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Pred. No. 2.8e-11;
0; Mismatches 559;
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/organism="Xenopus tropicalis"
/mol type="genomic DNA"
/strain="Nigerian frog"
/db_xref="texon:8364"
/clone="CH216-165P18"
                                                                                                                                                                                                                                           Washington University School of Medicine
Email: submissions@watson.wustl.edu
Insert Length: 175000 Std Error: 0.00
                                                                                       Xenopus tropicalis (western clawed frog)
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High quality sequence start: 265
High quality sequence stop: 497.
Location/Qualifiers
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                                               CL082000.1 GI:40537913
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Best Local Similarity 48.0%;
Matches 527; Conservative
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              481; Conservative
Best Local Similarity
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/organism="Sorghum propinguum"
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/db xref="taxon:13211"
/clone="SP Ba0091G12"
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/clone="SP BeloBAC11; Site_1: HindIII; Site_2: HindIII; Paterson lab BAC library (HindIII)"
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                       Email: http://genome.arizona.edu
POR PRimers
FORWARD: atc agc gcc cgc gat cc
BACKWARD: gta aaa cga cgg cca gtg
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Sag primer: atc agc ggc cgc gat cc
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Surghum propinguam

Sukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopaida; Poalee; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Sorghum.

E 1 (bases 1 to 1074)

Swing,R., Yu,Y., Kim,H.R., Collura,K., Pries,G., Currie,J.,
Soderlund,C. and Hatfield,J.
Sequencing of Sorghum BAC ends.
http://genome.arizona.edu/stc/sorghum

L Unpublished (2203)
Contect: Rod Wing
Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
85721-0088, USA
Tel: 520 626 1967
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Sequence 1, Appl Sequence 13, App Sequence 16493, Sequence 16494, Sequence 13248, Sequence 11794, Sequence 11794, Sequence 12699, Sequence 12699, Sequence 15851, Sequence 15851, Sequence 15851, Sequence 15851, Sequence 12387, Sequence 12387, Sequence 12725, Sequence 12387, Sequence 12387,

US-09-790-988-1 US-08-487-826B-13 US-09-949-016-16492 US-09-949-016-16493 US-09-949-016-116494 US-09-949-016-11348 US-09-949-016-11794 US-09-949-016-11599 US-09-949-016-115853 US-09-949-016-115853 US-09-949-016-115853 US-09-949-016-115853 US-09-949-016-115853 US-09-949-016-115853 US-09-949-016-115853 US-09-949-016-115853 US-09-949-016-115853 US-09-949-016-115853 US-09-949-016-11287

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Sequence 14164, Application US/09949016

Sequence 14164, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

FILE REFERENCE: CLOO1307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FESTES for Windows Version 4.0

SEQ ID NO 14164

LENGTH: 18773
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Pred. No. 5.9e-18;
0; Mismatches 544;
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Best Local Similarity 49.5
Matches 547; Conservative
US-09-949-016-14164/C
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US-09-949-016-14164
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ORGANISM: F
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Sequence 13, Appl Sequence 16492, A Sequence 16493, A Sequence 16494, A

US-09-949-016-16492 US-09-949-016-16493 US-09-949-016-16494 .08-487-826B-13

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15350, A 15507, A 15508, A 15129, A 1280, Ap 17067, A 12378, A

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Patent No. 6812339
GENERAL INFORMATION:
GRIERAL TINFORMATION:
GRIERAL TINFORMATION:
TITLE OF INVENTION:
WITH HUMAN DISEASE, METHODS OF DEFECTION AND USES THEREOF FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT PLING DATE: 2000-44-14
PRIOR FILING DATE: 2000-10-13
PRIOR PILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
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                                                                                                                                                                  Score 135.4; DB 4;
Pred. No. 2.3e-14;
0; Mismatches 466;
SEQ ID NOS: 207012
FastSEQ for Windows Version 4.0
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                                                                                              NAME/KEY: misc feature
LOCATION: (1)...(187169)
OTHER INFORMATION: n = A,T,C
                                                                                                                                                                  Query Match
Best Local Similarity 49.4%;
Matches 463; Conservative
                                                     TYPE: DNA
ORGANISM: Human
FEATURE:
                                                                                                                                        US-09-949-016-12776
           SOFTWARE: FastSE
SEQ ID NO 12776
LENGTH: 187169
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GENERAL INFORMATION:

APPLICANT: VERTER, J. Craig et al.

APPLICANT: VERTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
FILE REFERENCE: CLOO1307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-00-01-20

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR FILING DATE: 2000-00-03

PRIOR PILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 200-012

SOFTWARE: PRESEED for Windows Version 4.0

SEQ ID NO 14164

LENGTH: 18773
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Matches 505; Conservative
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Sequence 15940, Application US/09949016

Sequence 15940, Application US/09949016

Sequence 15940, Application US/09949016

Sequence 15940, Application US/09949016

FRENERL NUMBER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REPERENCE: CLO01307

CURRENT FILING DATE: 2000-01-14

FRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 191569
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6.7%; Score 135.4; DB 4; Length 191569;
Best Local Similarity 49.4%; Pred. No. 2.3e-14;
Matches 463; Conservative 0; Mismatches 466; Indels 8;
                                                         1478 ATTTTAAATATTTTATATTTACGAGAAAAAAATA 1514
                                                                                            464 TTTATATATATATATATTCAGAGAGAGAAGAGA 428
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LOCATION: (1)...(191569)
OTHER INFORMATION: n = A,T,C or G
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US-09-949-016-17067/c
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Patent No. 6833447

GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
APPLICANT: Wiegand, Roger C.
APPLICANT: Wiegand, Roger C.
APPLICANT: Wiegand, Roger C.
FILE REFERENCE: 38-10(15849)B
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                                                                                          ATCAATTTATAAAAATATTTTACTTTATATGTTTTTCACATTTTTGTTAAACAAATCAT
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US-09-902-540-1357/c
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Sequence 17057, Application US/09949016

Sequence 17057, Application US/09949016

Batent NO. 6812339

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOO1307

CURRENT APPLICATION NUMBER: US/09/949,016

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20
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                                                                                                                                                                                                                                                                                                                                    Length 612;
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CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 20/01-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
LENGTH: 612
                                                                                                                                                                                                                                             ; LOCATION: (1)..(612)
; OTHER INFORMATION: unsure at US-09-902-540-1357
                                                                                                                                                         TYPE: DNA
ORGANISM: Myxococcus xanthus
FEATURE:
NAME/KEY: unsure
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LOCATION: (1)...(119153)
OTHER INFORMATION: n = A,T,C or G
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Best Local Similarity 48.4'
Matches 474; Conservative
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LOCATION: (1)...(11915;
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6.1%; Score 122.4; DB 4;
Local Similarity 46.1%; Pred. No. 3.6e-12;
nes 520; Conservative 0; Mismatches 601;
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17067
LENGTH: 95255
                                                                                                                                                                                                                                                                                                  LOCATION: (1)...(95255)
OTHER INFORMATION: n = A,T,C or
                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature
                                                                                                                                                                                                                           ORGANISM: Human
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US-09-949-016-17067
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48.4%; Pred. No. 9.6e-11;
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RESULT 9
US-09-949-016-12423
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LENGTH: 29717
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Sequence 16284, Application US/09949016

Patent No. 681239

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICANTON NUMBER: US/09/949,016

CURRENT APPLICANTON NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FRASESEQ FOR Windows Version 4.0
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 1064 ----TATTTCCACTCATATATACACTCCAAAATTGGGGCATGCCTTTATCACTACTCT
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Sequence 12423 Application US/09949016
Fatent No. 6812339
GENERAL INFORMATION:
FAPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION:
FILE REFERENCE: CL001307
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FRICH FILING DATE: C000-04-14
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FRICH FILING DATE: C000-10-20
FRICH REPERENCE: C000-10-03
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Pred. No. 4.3e-10;
0; Mismatches 275; Indels
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TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(29717)
OTHER INFORMATION: n = A,T,C or
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Best Local Similarity 53.3%;
Matches 324; Conservative
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Sequence 17145, Application US/09949016

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CLOO1307

CURRENT APPLICATION NUMBER: US/09/949,016
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5.5%; Score 110; DB 4; Length 60
Best Local Similarity 53.3%; Pred. No. 4.6e-10;
Matches 324; Conservative 0; Mismatches 275; Indels
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 12423
LENGTH: 60376
                                                                                                         TACCTANA 47986
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                                                                        TYPE: DNA
ORGANISM: Human
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US-09-949-016-17145
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Pred. No. 5.4e-10;
0; Mismatches 521;
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-3
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SEQ ID NO 17145
                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 47.0%;
Matches 470; Conservative
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ASSOCIATED OF USES THEREOF
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                                                      757 ATAAGAAATAAATTTTGTAAATTTTTATTATCAATTTATAAAAATATTTATAAT
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Sequence 17145/c

Sequence 17145 Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSONTITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF FILE REFERENCE: CLOO1307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-04-14

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-30

PRIOR FILING DATE: 2000-10-31

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FASLESEQ for Windows Version 4.0

LENGTH: 30820
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0; Mismatches 524;
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Matches 483; Conservative
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US-09-949-016-17145
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Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF PILE REFERENCE: CL001307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      136758 ATATTTTTTATATATTTATATATATATTTGTATATATTTTATTTATTTATTTTATTTTATATTTT 136817
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     557 TATTACTTTTTTCTCTATTAGTTCTATTTTCAAATTATTATTATGCATATGTAA 616
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                                        TATGTTATTTTTTGATGTATGTATATTCGAATAAATCTAAATATATGATATGTTTTT
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5.1%; Score 105.8; DB 4; Length
Best Local Similarity 52.5%; Pred. No. 2.7e-09;
Matches 299; Conservative 0; Mismatches 267; Indels
                                                                                                                                                                               1442 ATAATTTTATAAGGATAAAAATATGATAAAAATAAATT 1480
                                                                                                                                                                                                   ACGTTTCCCATTTCCCACTTAATATGAAAAAAATACACT 6858
                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR PILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-0-06
SOFTWARE: PARELEQ for Windows Version 4.0
SOFTWARE: PARELEQ for Windows Version 4.0
SEQ ID NO 14624
LENGTH: 147382
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; LOCATION: (1)...(147382)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14654
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ORGANISM: Human
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US-09-949-016-14624
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Sequence 15349, Application US/09949016

Patent No. 681239
GENERAL INFORMATION:
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR PAPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,756
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FasteEG for Windows Version 4.0
SEQ ID NO 15349
                                607 GCATATGTAAAGTACATTATATTTTTGCTATATACTTAAATATTTCTAAATTATAAAAA
                                                                                                                                                                                                AAGACTGATATGAAAATTTATTCTTTTTAAAGCTATATCAT----TTTATATATACTTTT
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                                                                         547 ITAATTATTATATTACTTTTTCTCTATTCTATTAGTTCTATTTTCAAATTATTATTAT
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50.4%; Pred. No. 3.2e-09;
tive 0; Mismatches 276;
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Matches 284; Conservative
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US-09-949-016-15349
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Best Local
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US-09-949-016-15348
US-09-949-016-15348

Sequence 15348, Application US/09949016

Sequence 15348, Application US/09949016

Sequence 15348, Application US/09949016

Setting 1339

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: 10/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-00-08

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 20/0012

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 15348

LENGTH: 134987
                                                                                    ATGATATTTTTTATATAGGTTGTACACATAATTTTATAAGGATAAAAATATGATAAAA 1473
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               1174 CTCCTCAAGTGATTTCCAACTCAGCATTGGCATCTGATTCAGTATATCTATTGCAT
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                                                                                                                   1114 CTCTATCTCCTCCACTAAATCATTTAAATGAAACTGAAAAGCATTGGCAAGTCTCCTCCC
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Pred. No. 3.2e-09;
0; Mismatches 276;
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Best Local Similarity 50.4
Matches 284; Conservative
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Sequence 15350, Application US/09949016

Sequence 15350, Application US/09949016

Sequence 15350, Application US/09949016

GENERAL INFORMATION:

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-14-14

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 15350

LENGTH: 134987
                                                                                                                                                                             487 AAAAGAAATATTGTTTATATTCTTAATTAAAAATATTGTCCCTTCTAAATTTTCATATAG 546
                                                                                      GCATATGTAAAGTACATTATATTTTGCTATATACTTAAATATTTCTAAATTATTAAAAA 666
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Best Local Similarity 50.4
Matches 284; Conservative
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; ORGANISM: Human
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Search completed: September 1, 2005, 22:18:37 Job time : 254.78 secs